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GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 11:46:42 ; Search time 19.576 Seconds
(without alignments)
2384.805 Million cell updates/sec

Title: US-09-521-335-2
Perfect score: 1169
Sequence: 1 MLACICTVLWHLPAVPALNR.....KKMQPPAAAVTLHLGAHGF 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 671580
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTEMBL 21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1169	100.0	225	4	Q9UBD9 homo sapien
2	1136	97.2	225	11	Q9QZM3 mus musculus
3	150.5	12.9	215	13	Q9PUJ2 plethodon j
4	150.5	12.9	215	13	Q9PUJ1 plethodon j
5	150.5	12.9	215	13	Q9PUJ0 plethodon j
6	148.5	12.7	215	13	Q9PUI9 plethodon j
7	97.5	8.3	530	3	Q8X0E9 neurospora
8	94.5	8.1	318	4	Q96LS2 homo sapien
9	92	7.9	332	10	Q9MAU1 gmaul arabidopsis
10	92	7.9	423	11	Q9JHE4 mus musculus
11	92	7.9	455	11	Q9CWV7 mus musculus
12	90	7.7	423	11	Q9D8V6 mus musculus
13	89	7.6	733	16	Q91664 pseudomonas
14	88	7.5	771	2	Q9S3Q9 porphyromon
15	87	7.4	955	11	O88287 mus musculus
16	87	7.4	1561	11	O88286 mus musculus

17	86.5	7.4	640	16	O54153 streptomyce
18	85.5	7.3	1154	11	Q9Z1R2 mus musculus
19	85	7.3	127	11	O88841 mus musculus
20	84.5	7.2	294	11	Q9CPZ1 mus musculus
21	84.5	7.2	389	17	O9YA71 aeropyrum p
22	84	7.2	294	4	Q9NXX5 homo sapien
23	84	7.2	876	4	Q9P210 homo sapien
24	83.5	7.1	310	4	O9S159 homo sapien
25	83.5	7.1	5990	2	Q9RLP6 mycobacteri
26	83	7.1	222	2	Q9L584 streptococ
27	82.5	7.1	310	4	Q9UID0 homo sapien
28	82.5	7.1	542	16	Q9HTB5 pseudomonas
29	82	7.0	283	2	Q9ZB87 pseudomonas
30	82	7.0	611	16	Q98LP5 rhizobium l
31	82	7.0	721	4	Q96PC8 homo sapien
32	82	7.0	756	4	Q96PC7 homo sapien
33	82	7.0	1179	10	O65507 arabidopsis
34	82	7.0	2376	10	Q9FIN7 arabidopsis
35	81.5	7.0	396	2	Q9AF00 frankia sp.
36	81.5	7.0	476	11	Q8R363 mus musculus
37	81	6.9	328	15	Q9E125 human immun
38	81	6.9	328	15	Q9E122 human immun
39	81	6.9	924	2	Q9X582 rhodothermu
40	80.5	6.9	200	16	Q8YBB1 brucella me
41	80.5	6.9	305	4	Q9H7R6 homo sapien
42	80.5	6.9	466	4	Q96CD4 homo sapien
43	80.5	6.9	512	13	Q9FSM0 xenopus lae
44	79.5	6.8	433	10	Q9FI78 arabidopsis
45	79.5	6.8	924	2	Q9ZIG3 rhodothermu

ALIGNMENTS

RESULT 1

Q9UBD9	PRELIMINARY;	PRT;	225 AA.
ID	Q9UBD9		
AC	Q9UBD9;		
DT	01-MAY-2000 (TEMBLrel. 13, Created)		
DT	01-MAY-2000 (TEMBLrel. 13, Last sequence update)		
DT	01-DEC-2001 (TEMBLrel. 19, Last annotation update)		
DE	Neurotrophin-1/B-cell stimulating factor-3 (Cardiotrophin-like cytokine) (Similar to cardiotrophin-like cytokine, neurotrophin-1/B-cell stimulating factor-3).		
DE	Neurotrophin-1/B-cell stimulating factor-3.		
GN	CtC.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99432254; PubMed=10500198;		
RA	Senaldi G., Varnum B.C., Sarmiento U., Starnes C., Lile J., Scully S., Guo J., Elliott G., McNinch J., Shaklee C.L., Freeman D., Manu F., Simonet W.S., Boone T., Chang M.-S.;		
RA	"Novel neurotrophin-1/B cell-stimulating factor-3: A cytokine of the IL-6 family."		
RT	Proc. Natl. Acad. Sci. U.S.A. 96:11458-11463(1999).		
RL	[2]		
RN	SEQUENCE FROM N.A.		
RP	MEDLINE=99382254; PubMed=10448081;		
RX	Shi Y., Wang W., Yourey P.A., Gohari S., Zukauskas D., Zhang J., Ruben S., Alderson R.F.;		
RA	"Computational EST database analysis identifies a novel member of the neurotrophic cytokine family."		
RT	Biochem. Biophys. Res. Commun. 262:132-138(1999).		
RL	[3]		
RN	SEQUENCE FROM N.A.		
RP	Hu X., Xu Y., Zhang B., Peng X., Yuan J., Qiang B.;		
RA	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=KIDNEY;		

RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF176912; AAF00992.1; -
DR EMBL; AF172854; AAD54284.1; -
DR EMBL; AF176911; AAF00991.1; -
DR EMBL; AY049779; AAL15436.1; -
DR EMBL; BC012939; AAL12939.1; -
SQ SEQUENCE 225 AA; 25176 MW; E2DD4B628083B55 CRC64;

Query Match 100.0%; Score 1169; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 2.5e-101; Indels 0; Gaps 0;
Matches 215; Conservative 0; Mismatches 0;

Qy 1 MLACICTVWHLPAVPAALNRRTGDPGPGPSIQKTYDLYLEHQLRSLAGTYLNYLGGPPFN 60
Db 11 MLACICTVWHLPAVPAALNRRTGDPGPGPSIQKTYDLYLEHQLRSLAGTYLNYLGGPPFN 70
Qy 61 EPDFNPPRLGAEATLPRAVTVLEWVRSNDKRLTONYEAYSHLLCYLRGLNRQAATAELR 120
Db 71 EPDFNPPRLGAEATLPRAVTVLEWVRSNDKRLTONYEAYSHLLCYLRGLNRQAATAELR 130
Qy 121 RSLAHFCTSLQGLGSIAGVMAALGYPLPQPLGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
Db 131 RSLAHFCTSLQGLGSIAGVMAALGYPLPQPLGTEPTWTPGPAHSDFLQKMDDFWLLKE 190
Qy 181 LQTLWRSKDFNRLKKKMQPPAAVTLHLGAHGF 215
Db 191 LQTLWRSKDFNRLKKKMQPPAAVTLHLGAHGF 225

RESULT 2
Q9QZM3 Q9QZM3 PRELIMINARY; PRT; 225 AA.
AC Q9QZM3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Neurotrophin-1/B-cell stimulating factor-3.
GN BSG3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=99432254; PubMed=10500198;
RA Senaldi G., Varnum B.C., Sarmiento U., Starnes C., Lile J., Scully S.,
Guo J., Elliott G., McNinch J., Shaklee C.L., Freeman D., Manu F.,
Simonet W.S., Boone T., Chang M.-S.;
"Novel neurotrophin-1/B cell-stimulating factor-3: a cytokine of the
IL-6 family";
Proc. Natl. Acad. Sci. U.S.A. 96:11458-11463(1999).
RL EMBL; AF176913; AAF00993.1; -
DR MGD; MGI:1930088; Bsf3.
SQ SEQUENCE 225 AA; 25261 MW; 68B1FEAB7F1A950 CRC64;

Query Match 97.2%; Score 1136; DB 11; Length 225;
Best Local Similarity 96.7%; Pred. No. 3.1e-98; Indels 0; Gaps 0;
Matches 208; Conservative 3; Mismatches 4;

Qy 1 MLACICTVWHLPAVPAALNRRTGDPGPGPSIQKTYDLYLEHQLRSLAGTYLNYLGGPPFN 60
Db 11 MLACICTVWHLPAVPAALNRRTGDPGPGPSIQKTYDLYLEHQLRSLAGTYLNYLGGPPFN 70
Qy 61 EPDFNPPRLGAEATLPRAVTVLEWVRSNDKRLTONYEAYSHLLCYLRGLNRQAATAELR 120
Db 71 EPDFNPPRLGAEATLPRAVTVLEWVRSNDKRLTONYEAYSHLLCYLRGLNRQAATAELR 130
Qy 121 RSLAHFCTSLQGLGSIAGVMAALGYPLPQPLGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
Db 131 RSLAHFCTSLQGLGSIAGVMAALGYPLPQPLGTEPTWTPGPAHSDFLQKMDDFWLLKE 190
Qy 181 LQTLWRSKDFNRLKKKMQPPAAVTLHLGAHGF 215

Db 191 LQTLWRSKDFNRLKKKMQPPAAVTLHLGAHGF 225

RESULT 3
Q9PUJ2 Q9PUJ2 PRELIMINARY; PRT; 215 AA.
AC Q9PUJ2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Receptivity factor isoform 1 precursor.
GN PRF.
OS Plethodon jordani (Salamander).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;
OC Plethodon.
OX NCBI_TaxID=8336;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99420364; PubMed=10489368;
RA Rollmann S.M., Houck L.D., Feldhoff R.C.;
"Proteinaceous pheromone affecting female receptivity in a terrestrial
salamander";
Science 285:1907-1909(1999).
RL EMBL; AF181480; AAF01025.1; -
DR Signal.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
SQ SEQUENCE 215 AA; 24138 MW; B1906BB666335738 CRC64;

Query Match 12.9%; Score 150.5; DB 13; Length 215;
Best Local Similarity 26.2%; Pred. No. 3.3e-06; Indels 7; Gaps 3;
Matches 42; Conservative 31; Mismatches 80;

Qy 46 SLACTYLNLYLGGPPNEPDPNPPRLGAEATLPRAVTVLEWVRSNDKRLTONYEAYSHLLC 105
Db 55 SLLEPTLYSFGAGPLSDPDYQLPHIKVANLPTAAMDYDTFMKQTDTRLNNNLYFSALVE 114
Qy 106 YLR-GLNRQ----AATAELRRSLAHFCTSLQGLGSIAGVMAALGYPLPQPLGTEPTWT 160
Db 115 FLKAMTEQEDLNPAELSLKAKPEEAMNSNTLSKISDINTQGMSTITLP--KPLV 172
Qy 161 PGPAHSDFLQKMDDFWLLKELOTLWRSKDFNRLKKKMQ 200
Db 173 PFEGSAVFRKKLGGVVCKEYKERVLLTKRDFEFLAKKYQ 212

RESULT 4
Q9PUJ1 Q9PUJ1 PRELIMINARY; PRT; 215 AA.
AC Q9PUJ1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Receptivity factor isoform 2 precursor.
GN PRF.
OS Plethodon jordani (Salamander).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;
OC Plethodon.
OX NCBI_TaxID=8336;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99420364; PubMed=10489368;
RA Rollmann S.M., Houck L.D., Feldhoff R.C.;
"Proteinaceous pheromone affecting female receptivity in a terrestrial
salamander";
Science 285:1907-1909(1999).
RL EMBL; AF181481; AAF01026.1; -
DR Signal.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
SQ SEQUENCE 215 AA; 24080 MW; B341B8B7B4E28438 CRC64;

```

Db 84 ---SERLRQDAALGALPALLDAVRRRQAEINPRAPRLRLSLEDAARQVRAAGAVETVL 140
Qy 142 AALGP---PLPOPLPGTEPTWPCPAHSDFLOKMDDFWLLKELQTLWLRSAKDPNRL 195
Db 141 AALGAARGPPEPV-ATSAULTSNAAGVFSKVLGHVCGLYGWNVRTEGDLGQL 197

RESULT 2
CTF1_MOUSE
ID CTf1_MOUSE STANDARD; PRT; 203 AA.
AC Q60753;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Cardiotrophin-1 (CT-1).
GN CTF1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RX MEDLINE=9516785; PubMed=7862649;
RA Pennica D., King K.L., Shaw K.J., Luis E., Rullamas J., Luoh S.-M.,
RA Darbonne W.C., Knutson D.S., Yen R., Chien K.R., Baker J.B.,
RA Wood W.I.;
RT "Expression cloning of cardiotrophin 1, a cytokine that induces
RT cardiac myocyte hypertrophy."
RL Proc. Natl. Acad. Sci. U.S.A. 92:1142-1146(1995).
CC -!- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPHY IN VITRO. BINDS TO
CC AND ACTIVATES THE LEUKEMIA INHIBITORY FACTOR RECEPTOR (LIF
CC RECEPTOR)/GP 130 RECEPTOR COMPLEX.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, SKELETAL MUSCLE,
CC LIVER, LUNG AND KIDNEY. LOWER LEVELS IN TESTIS AND BRAIN. NO
CC EXPRESSION IN SPLEEN.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL; U18366; AAC52173.1; -.
MGD; MGI:105115; Ctf1.
Cytokine.
SEQUENCE 203 AA; 21509 MW; 8B3D414A0B3B232F CRC64;

Query Match 10.1%; Score 118.5; DB 1; Length 203;
Best Local Similarity 28.8%; Pred. No. 0.00046;
Matches 51; Conservative 21; Mismatches 88; Indels 17; Gaps 5;

Qy 30 IOKTYDLYLEHQLRSAGTYLNYLGGPFNPFDPNPRPL---GAETLPRAVTLDEWMS 86
Db 27 IQQTHNLARLLTKYAEQLLEEVVQOGEFGPLGPGFPRLPLAGLSGPAHPV--- 83
Qy 87 LNDKLRLTQNYEAYSHLLCYLRLGNRAA-----TAELESLAHFCTSLQGLLGSITAGYM 141
Db 84 ---SERLRQDAALSVLPALLDAVRRRQAEINPRAPRLRLSLEDAARQVRAAGAVETVL 140
Qy 142 AALGPPL--PQPLPGTEPT-WTPGPAHSDFLOKMDDFWLLKELQTLWLRSAKDPNRL 195
Db 141 AALGAARGPPEPVATLTFTANSTAGIFSAGVLGHVCGLYGWNVRTEGDLGQL 197

RESULT 3
CST_MOUSE
ID CST_MOUSE STANDARD; PRT; 423 AA.
AC Q9JHE4; Q9D8V6;

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DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Galactosylceramide sulfotransferase (EC 2.8.2.11) (GalCer
DE sulfotransferase) (Cerebroside sulfotransferase) (3'-
DE phosphoadenylylsulfate:galactosylceramide 3'-sulfotransferase)
DE (3'-phosphoadenosine-5'-phosphosulfate:GalCer sulfotransferase).
GN CST OR GCST.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RX SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RA TISSUE=Kidney;
RA PubMed=10727929;
RA Hirahara Y., Tsuda M., Wada Y., Honke K.;
RT "CDNA cloning, genomic cloning, and tissue-specific regulation of
RT mouse cerebroside sulfotransferase."
RL Eur. J. Biochem. 267:1909-1917(2000).
[2]
RX SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Pancreas;
RA MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
[3]
RX SEQUENCE FROM N.A.
RA TISSUE=Colon;
RA Strausberg R.;
RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
[4]
RX FUNCTION.
RA PubMed=11917099;
RA Honke K., Hirahara Y., Dupree J., Suzuki K., Popko B., Fukushima K.,
RA Fukushima J., Nagasawa T., Yoshida N., Wada Y., Taniguchi N.;
RT "Paranodal junction formation and spermatogenesis require
RT sulfoglycolipids."
RL Proc. Natl. Acad. Sci. U.S.A. 99:4227-4232(2002).
CC -!- FUNCTION: Catalyzes the sulfation of membrane glycolipids. Seems
CC to prefer beta-glycosides at the nonreducing termini of sugar
CC chains attached to a lipid moiety. Catalyzes the synthesis of
CC HSO3-3-galactosylceramide (sulfatide), a major lipid component of
CC the myelin sheath and of HSO3-3-monogalactosylalkylglycerol
CC (seminolipid), present in spermatozoa. Also acts on
CC lactosylceramide, galactosyl 1-alkyl-2-sn-glycerol and galactosyl
CC diacylglycerol (in vitro).
CC -!- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate + a
CC galactosylceramide = adenosine 3',5'-bisphosphate +
CC galactosylceramide sulfate.
CC -!- CATALYTIC ACTIVITY: 3'-phosphoadenylylsulfate +
CC monogalactosylalkylglycerol = adenosine 3',5'-bisphosphate +
CC monogalactosylalkylglycerol sulfate.
CC -!- PATHWAY: Sphingolipid and glycerolipid biosynthesis.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Golgi membrane (By

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GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 11:41:52 ; Search time 6.192 Seconds
(without alignments)
1440.150 Million cell updates/sec

Title: US-09-521-335-2

Perfect score: 1169

Sequence: 1 MLACLCTVLWLPVAPALNR.....KKKMQPPAAAVTLHLGAHGF 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	124.5	10.7	203	1 CTF1_RAT	Q63086 rattus norv
2	118.5	10.1	203	1 CTF1_MOUSE	Q60753 mus musculu
3	94	8.0	423	1 CST_MOUSE	Q9jhe4 m galactosy
4	91.5	7.8	201	1 CTF1_HUMAN	Q16619 homo sapien
5	91	7.8	195	1 CNTF_CHICK	Q02011 gallus gall
6	91	7.8	1182	1 HAIR_MOUSE	Q61645 mus musculu
7	89.5	7.7	1313	1 MIPI_SCHPO	P87141 schizosacch
8	87.5	7.5	1181	1 HAIR_RAT	P97609 rattus norv
9	86	7.4	1009	1 M2B2_HUMAN	O9y2e5 homo sapien
10	85.5	7.3	560	1 PHAC_PSEOL	P26496 pseudomonas
11	84	7.2	200	1 CNTF_PIG	O02732 sus scrofa
12	84	7.2	619	1 NXF1_HUMAN	Q9ubn9 homo sapien
13	83	7.1	452	1 TLL_DROME	P18102 drosophila
14	81.5	7.0	1189	1 HAIR_HUMAN	Q43593 homo sapien
15	81	6.9	291	1 MYC2_MYCTU	Q10515 mycobacteri
16	81	6.9	724	1 P85B_BOVIN	P23726 bos taurus
17	80.5	6.9	294	1 HUPK_RHOCA	P20797 rhodobacter
18	80.5	6.9	870	1 BCAL_HUMAN	P56945 homo sapien
19	80	6.8	200	1 CNTF_RAT	P20294 rattus norv
20	79	6.8	1621	1 ALK_MOUSE	P97793 mus musculu
21	78.5	6.7	390	1 YL2B_STRCO	P40181 streptomyc
22	78.5	6.7	1102	1 CARB_STRCO	O9kxr6 streptomyc
23	78	6.7	3680	1 DMD_CANFA	O97592 canis fami
24	77	6.6	586	1 UL84_HCNVA	P16727 human cyto
25	77	6.6	587	1 UL84_HCMVT	P29839 human cyto
26	76.5	6.5	572	1 SYM_AERPE	O9ycv3 aeropyrum p
27	76.5	6.5	618	1 NXF1_RAT	O88984 rattus norv
28	76.5	6.5	995	1 M2B2_PIG	Q28949 sus scrofa
29	76	6.5	1001	1 FTFX_MOUSE	P80560 mus musculu
30	76	6.5	1132	1 BAT3_HUMAN	Q46379 homo sapien
31	75.5	6.5	422	1 Y140_HUMAN	Q14153 homo sapien
32	75.5	6.5	830	1 VPP3_HUMAN	Q13488 h vacuolar
33	75	6.4	199	1 CNTF_RABIT	P14188 oryctolagus

RESULT 1
CTF1_RAT
ID CTF1_RAT STANDARD; PRT; 203 AA.

AC O63086;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Cardiotrophin-1 (CT-1).

GN CTF1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Wistar; TISSUE=Heart;

RX MEDLINE=96193659; PubMed=8604995;

RA Ishikawa M., Saito Y., Miyamoto Y., Kuwahara K., Ogawa E.,

RA Nakagawa O., Harada M., Masuda I., Nakao K.;

RT "cDNA cloning of rat cardiotrophin-1 (CT-1): augmented expression of

CT-1 gene in ventricle of genetically hypertensive rats.";

RL Biochem. Biophys. Res. Commun. 219:377-381(1996).

CC -!- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPHY IN VITRO. BINDS TO

CC AND ACTIVATES THE LEUKEMIA INHIBITORY FACTOR RECEPTOR (LIF

CC RECEPTOR)/GP 130 RECEPTOR COMPLEX.

CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -!- TISSUE SPECIFICITY: EXPRESSED IN THE VENTRICLE AND ATRIUM OF ADULT

CC RATS. ALSO DETECTED IN THE LUNG, KIDNEY, LIVER, SKELETAL MUSCLE,

CC STOMACH AND URINARY BLADDER. NOT DETECTED IN BRAIN, COLON, TESTIS,

CC SPLEEN OR THYMUS. OVEREXPRESSED IN THE VENTRICLES IN THE CASE OF

CC HYPERTENSION AND HYPERTROPHY.

CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC

CC EMBL; D78591; BAA11427.1; -.

CC InterPro; IPR001581; LIF_OSM.

DR SMART; SM00080; LIF_OSM; 1.

KW Cytokine.

SQ SEQUENCE 203 AA; 21439 MW; DF8B921A2FA1C832 CRC64;

Query Match 10.7%; Score 124.5; DB 1; Length 203;
Best Local Similarity 28.1%; Pred. No. 0.00012;
Matches 50; Conservative 24; Mismatches 85; Indels 19; Gaps 5;

QY 30 IQTYDLTRVLEQLSLAGTLYNLGPPENEDFNPPRI---GAETLPRATVDLEWRS 86

DB 27 IROTHNLRLLTKYAOQLLEBYQQQGEPPGLPGFSPRLPLAGLSGAPSPAGLPV--- 83

QY 87 LNDKLRLTQNYEAYSHLLCYLRGLNRQAA-----TABLRRLSLAHFCTSLQGLLSIAGVM 141

ALIGNMENTS

C;Keywords: cytokine; glycoprotein
F;164/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.1%; Score 118.5; DB 2; Length 203;
Best Local Similarity 28.8%; Pred. No. 0.0014;
Matches 51; Conservative 21; Mismatches 88; Indels 17; Gaps 5;

Qy 30 IQKTYDLTRYLEHQLRSAGTYLNYLGGPFNEPDPNPRL---GAETLPRAVDLEWRS 86
Db 27 IROTHNLARLLTKYAEQLLEEIVQOQGFGLPGSPRLPLAGLSGAPSHAGLPV--- 83

Qy 87 LNDKRLQNTQYAYSHLLCYLRLGNRQAA-----TAEIARRSLAHFCTSLQGLGSIAGVM 141
Db 84 ---SRLRQDAALSVLPALLDAVRRQAEINPRAPRLRLSLRLEDAARQVRLGAIVETVL 140

Qy 142 AALGYPL--PQPLPCTET--WTPGPAHSDFLQKDDFWLLKELQTLWRSKDFNRL 195
Db 141 AALGAARGGPEPVTVATLFTANSTAGIFSARVILGFHVCGLYGEWSRTEGDLGQL 197

32
hypochemical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: G86182
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: G86182
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-332 <STO>
A;Cross-references: GB:AB005172; NID:g7211973; PIDN:AAF40444.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1

Query Match 7.9%; Score 92; DB 2; Length 332;
Best Local Similarity 26.4%; Pred. No. 0.76;
Matches 58; Conservative 24; Mismatches 72; Indels 66; Gaps 13;

13 PAVPALNRTGDPGPGSIQKTYDLTRYLEHQLRSAGTYLNY----- 54
Db 113 FSVTGNLSGYP-PRPSP--TYDGPYEQRQWESLLOQFIRENPQIRPLRLGLGSPVG 169

Qy 55 LGPPNEPDPNPRLGAETLPRAVDLEWRSNDKRLQNTQYAYSHLLCYLRLGNRQAA 114
Db 170 LGPIRASQFLQPRVAPP--PTSILD---TSNRKAR-----SKDGLAVVRG--RKV 215

Qy 115 ATAEIARRSL-----AHFCTSLQGLGSIAGVMAALGYPLPQPLP---GTEPTWT 160
Db 216 RITEGSSSLYSLGRSMLKNGAHV-----GIQPRSGIMK---PLPKPLPVLDTTTSVP 266

Qy 161 PGPAHSDFLQKDDFWLLKELQTLWRSKDFNRLKKKMQ 200
Db 267 DDPDESADKEDBEAVKQL-----SEKOL--LKRHIE 298

RESULT 4
G02312
cardiotrophin-1 - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998
C;Accession: G02312
R;Wood, W.I.

submitted to the EMBL Data Library, December 1995
A;Reference number: H01035
A;Accession: G02312
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-201 <WOO>
A;Cross-references: EMBL:U43030; NID:g1151149; PID:g1151150
C;Genetics:
A;Gene: GDB:CTF1; CT-1
A;Cross-references: GDB:567078
A;Map position: ip22-1p22

Query Match 7.8%; Score 91.5; DB 2; Length 201;
Best Local Similarity 25.9%; Pred. No. 0.45;
Matches 45; Conservative 24; Mismatches 92; Indels 13; Gaps 5;

Qy 30 IQKTYDLTRYLEHQLRSAGTYLNYLGGPFNEPDPNPRLGAETLPRAVDLEWRSND 89
Db 27 IROTHSLAHLTKYAEQLQOEYVOLQDGFGLPGSPRLPVAGL--SAPAPSHAGLPVHE 85

Qy 90 KRLQNTQYAYSHLLCYLRLGNRQAA-----TAEIARRSLAHFCTSLQGLGSIAGVMAAL 144
Db 86 RLRLI--DAALAAALPPLLDVACRQAEINPRAPRLRLRLEDAARQALGAIVETLAL 143

Qy 145 GYPLPQPLPCTET---TWTPGPAHSDFLQKDDFWLLKELQTLWRSKDFNRL 195
Db 144 G--AANRGPRAEPPAATAASAATGVFPKVLGLRVCGLYREWLRSRTGDLGQL 195

RESULT 5
JH0680
ciliary neurotrophic factor - chicken
N;Alternate names: growth-promoting activity protein
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000
C;Accession: JH0680; PQ0057
R;Leung, D.W.; Parent, A.S.; Cachianes, G.; Esch, F.; Coulombe, J.N.; Nikolic, K.; Ecker,
Neuron 8, 1045-1053, 1992
A;Title: Cloning, expression during development, and evidence for release of a trophic
A;Reference number: JH0680; MUID:92304573; PMID:1610564
A;Accession: JH0680
A;Molecule type: mRNA
A;Residues: 1-195 <LEU>
A;Cross-references: GB:M80827; NID:g211822; PIDN:AAA48784.1; PID:g211823
R;Eckstein, F.P.; Esch, F.; Holbert, T.; Blacher, R.W.; Nishi, R.
Neuron 4, 623-631, 1990
A;Title: Purification and characterization of a trophic factor for embryonic peripheral
A;Reference number: PQ0057; MUID:90211978; PMID:2322465
A;Accession: PQ0057
A;Molecule type: protein
A;Residues: 155-166, X, 168-175 <ECK>
A;Experimental source: sciatic nerves
C;Comment: This is a neurotrophic protein.
C;Superfamily: ciliary neurotrophic factor
C;Keywords: growth factor

Query Match 7.8%; Score 91; DB 2; Length 195;
Best Local Similarity 27.3%; Pred. No. 0.48;
Matches 51; Conservative 21; Mismatches 83; Indels 32; Gaps 9;

Qy 36 LTRYLEHQLRSAGTYLNYLGGPFNEPDPNPRLGAETLPRAVDLEWRSNDKRLQTL 95
Db 23 LARKMSDVTDLDIYVERQ-----LDASISVAADVGVPTAAV--ERWASQTGTQRLLD 75

Qy 96 N---YEAYSHLLCYLRLGNRQAA-----ATAELRRSLA-----HFCTSLQGLGSIAGVMA 142
Db 76 NLAAVRAFTLLAQMLEBQRELLGDTDAELGPALAAAMLQVSAFVYHLEEL-----ELE 130

Qy 143 ALGYPLPQPLPCTETPTWTPGPAH--SDFLOKDDFWLLKELQTLWRSKDFNRLKKKMQ 201
Db 131 SRGAPAE---GSEF---PAPPRLSLFEQKRLGLRVLRLELAQNAVRSVRDLRQLSKHGPG 184

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 11:48:13 ; Search time 9.632 Seconds
(without alignments)
2145.858 Million cell updates/sec

Title: US-09-521-335-2
Perfect score: 1169
Sequence: 1 MLACLCVLMHLPVAPALNR.....KKMKQPPAAAVTLHLGAHF 215
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	124.5	10.7	203	JC4645	cardiotrophin-1 -
2	118.5	10.1	203	I49153	cardiotrophin-1 -
3	92	7.9	332	G86182	hypothetical prote
4	91.5	7.8	201	G02312	cardiotrophin-1 -
5	91	7.8	195	JH0680	ciliary neurotroph
6	91	7.8	1182	I48378	hairless protein -
7	89.5	7.7	1313	T38943	probable guanine n
8	89	7.6	733	D83588	conserved hypothet
9	87	7.4	955	T00247	zinc finger protei
10	87	7.4	1561	T00248	zinc finger protei
11	86.5	7.4	640	T34916	transferase - Stre
12	85.5	7.3	560	C38604	poly(3-hydroxyvalk
13	84.5	7.2	389	F72511	probable cystathio
14	83	7.1	452	A35602	tailless (c1l) pro
15	82.5	7.1	542	A82965	hypothetical prote
16	82	7.0	1179	T04584	TMV resistance pro
17	81.5	7.0	723	B38749	3-phosphatidylinos
18	80.5	6.9	200	A23633	hypothetical prote
19	80.5	6.9	512	D21171	activin receptor S
20	80	6.8	200	UNR7CF	ciliary neurotroph
21	79	6.8	353	A81823	hypothetical prote
22	79	6.8	559	G71327	probable apolipop
23	79	6.8	812	T34180	hypothetical prote
24	79	6.8	1220	A40125	exodeoxyribonuclea
25	79	6.8	1621	T30200	protein-tyrosine k
26	78.5	6.7	390	T35509	hypothetical prote
27	78.5	6.7	426	A10287	conserved hypothet
28	78.5	6.7	460	D75493	cell division cycl
29	78	6.7	254	T08755	yes-associated pro

30	78	6.7	272	2	T35231	hypothetical prote
31	77.5	6.6	7463	2	T36248	CDA peptide synthe
32	77	6.6	520	2	B75332	extracellular solu
33	77	6.6	586	1	WMBEDE	65K early nonstruc
34	77	6.6	587	1	WMBETE	65K early nonstruc
35	77	6.6	733	2	F82965	hypothetical prote
36	76.5	6.5	310	2	A82734	conserved hypothet
37	76.5	6.5	338	2	T45394	hypothetical prote
38	76.5	6.5	522	2	D87123	conserved hypothet
39	76.5	6.5	572	2	B72714	probable methionyl
40	76.5	6.5	837	2	T12514	hypothetical prote
41	76.5	6.5	1006	2	T42762	probable alpha-man
42	76	6.5	531	2	B83422	probable serine/th
43	76	6.5	1007	2	E72489	hypothetical prote
44	76	6.5	1031	2	F83561	probable DNA polym
45	76	6.5	1132	2	A35098	MHC class III hist

ALIGNMENTS

RESULT 1
JC4645
cardiotrophin-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 20-Jun-2000
C:Accession: JC4645
R:Ishikawa, M.; Saito, Y.; Miyamoto, Y.; Kuwahara, K.; Ogawa, E.; Nakagawa, O.; Harada, N
Biochem. Biophys. Res. Commun. 219, 377-381, 1996
A>Title: cDNA cloning of rat cardiotrophin-1 (CT-1): Augmented expression of CT-1 gene in
A:Reference number: JC4645; MUID:96193659; PMID:8604995
A:Accession: JC4645
A:Molecule type: mRNA
A:Residues: 1-203 <1SH>
A:Cross-references: DDBJ:D78591; NID:gi256926; PIDN:BAA11427.1; PID:gi256927
C:Genetics:
A:Gene: CT-1
C:Keywords: cardiac muscle; cytokine; heart

Query Match	10.7%;	Score	124.5;	DB 2;	Length	203;			
Best Local Similarity	28.1%;	Pred. No.	0.00039;						
Matches	50;	Conservative	24;	Mismatches	85;	Indels	19;	Gaps	5;
QY	30	IKQTYDLTRYLEHQLRSAGTYLNYLGGPPNFDPNPRL---GAETLPRAVDLEWVRS	86						
Db	27	IROTHNLARLLTKYADQLLEEYVQQQGEFGLPGFPFRLPLAGLGGPAPSHAGLPV---83							
QY	87	LNDKLRLTQNYEAYSHLLCYLRGLNRQAA-----TAELESLAHFCTSLQGLLGSAGVM	141						
Db	84	---SERLRQDAASALPALLDAVRRRQAEINPRAPRLRLSLDEAARQVRALGAAVETVL	140						
QY	142	AALGY----PLPQPLPGTEPTWTPGPAHSDFLOKMDDFWLLKELQTLWRSKDFNRL	195						
Db	141	AALGAAARGVPPEPV-ATSALFTSNSAAGVFSAKVLGLHVCGLYGEWVSRTGDLQOL	197						

RESULT 2
I49153
cardiotrophin-1 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
R:Pennica, D.; King, K.L.; Shaw, K.J.; Luis, E.; Rullamas, J.; Luoh, S.; Darbonne, W.C.;
Proc. Natl. Acad. Sci. U.S.A. 92, 1142-1146, 1995
A>Title: Expression cloning of cardiotrophin 1, a cytokine that induces cardiac myocyte
A:Reference number: I49153; MUID:95166785; PMID:7862649
A:Accession: I49153
A>Status: nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-203 <RES>
A:Cross-references: EMBL:U18366; NID:g710331; PIDN:AAC52173.1; PID:g710332
C:Genetics:
A:Gene: ctcf1

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 11:49:27 ; Search time 8.256 Seconds
(without alignments)
1200.314 Million cell updates/sec

Title: US-09-521-335-2
Perfect score: 1169
Sequence: 1 MLACLTVMHLPALNR.....KKKMPAAAVTLHLGAHGF 215

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 199416 seqs, 46092074 residues
Total number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA.*
- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
 - 10: /cgn2_6/ptodata/1/pubpaa/US05_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1169	100.0	225	10 US-09-931-704-2	Sequence 2, Appli
2	1136	97.2	225	10 US-09-931-704-5	Sequence 5, Appli
3	885	75.7	164	10 US-09-864-761-40014	Sequence 40014, A
4	118.5	10.1	203	10 US-09-896-856-3	Sequence 3, Appli
5	91.5	7.8	201	10 US-09-901-540-3	Sequence 3, Appli
6	91.5	7.8	201	10 US-09-896-856-8	Sequence 8, Appli
7	91.5	7.8	201	10 US-09-901-257-3	Sequence 3, Appli
8	91	7.8	195	10 US-09-770-361-5	Sequence 5, Appli
9	91	7.8	1182	9 US-10-024-368-6	Sequence 6, Appli
10	90	7.7	232	10 US-09-810-052-2	Sequence 2, Appli
11	90	7.7	242	9 US-10-000-776-2	Sequence 2, Appli
12	90	7.7	242	9 US-09-791-497-2	Sequence 2, Appli
13	90	7.7	243	9 US-10-000-776-6	Sequence 6, Appli
14	90	7.7	243	9 US-09-791-497-8	Sequence 8, Appli
15	90	7.7	243	10 US-09-810-052-5	Sequence 5, Appli
16	87.5	7.5	1207	9 US-10-024-368-5	Sequence 5, Appli
17	82	7.0	200	10 US-09-770-361-8	Sequence 8, Appli
18	81.5	7.0	218	10 US-09-893-737-28	Sequence 28, Appli
19	81.5	7.0	984	9 US-10-024-368-2	Sequence 2, Appli

20	81.5	7.0	1189	9 US-10-024-368-4	Sequence 4, Appli
21	81	6.9	200	10 US-09-770-361-6	Sequence 6, Appli
22	79	6.8	418	9 US-09-946-807-3	Sequence 3, Appli
23	79	6.8	418	10 US-09-795-668-3	Sequence 3, Appli
24	79	6.8	418	10 US-09-795-686-3	Sequence 3, Appli
25	77.5	6.6	200	10 US-09-770-361-10	Sequence 10, Appli
26	77.5	6.6	379	9 US-09-860-846-16	Sequence 16, Appli
27	77.5	6.6	379	10 US-09-861-289-16	Sequence 16, Appli
28	77.5	6.6	625	10 US-09-771-161A-242	Sequence 242, App
29	77.5	6.6	625	10 US-09-771-161A-243	Sequence 243, App
30	77.5	6.6	3782	9 US-09-860-846-4	Sequence 4, Appli
31	77.5	6.6	3782	10 US-09-861-289-4	Sequence 4, Appli
32	77	6.6	439	12 US-10-078-929-60	Sequence 60, Appli
33	76	6.5	348	10 US-09-730-617-2	Sequence 2, Appli
34	76	6.5	416	9 US-10-124-429-2	Sequence 2, Appli
35	76	6.5	451	10 US-09-764-864-1344	Sequence 1344, Ap
36	75.5	6.5	1040	9 US-09-988-626-238	Sequence 238, App
37	75.5	6.5	1040	9 US-09-988-687-238	Sequence 238, App
38	75	6.4	199	10 US-09-770-361-3	Sequence 3, Appli
39	75	6.4	917	10 US-09-815-242-5603	Sequence 5603, Ap
40	75	6.4	920	10 US-09-815-242-12181	Sequence 12181, A
41	75	6.4	920	10 US-09-815-242-12995	Sequence 12995, A
42	75	6.4	920	10 US-09-815-242-13148	Sequence 13148, A
43	75	6.4	1820	10 US-09-827-949-2	Sequence 2, Appli
44	73.5	6.3	1009	8 US-08-987-689A-2	Sequence 2, Appli
45	72.5	6.2	231	9 US-10-000-776-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-931-704-2
; Sequence 2, Application US/09931704
; Patent No. US20020041873A1
; GENERAL INFORMATION:
; APPLICANT: Senaldi, Giorgio
; TITLE OF INVENTION: Methods and Compositions for Treating IGE-Related Disease Using Nt
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: A-695
; CURRENT APPLICATION NUMBER: US/09/931,704
; CURRENT FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: US 60/226,436
; PRIOR FILING DATE: 2000-08-18
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-931-704-2

Query Match	100.0%;	Score 1169;	DB 10;	Length 225;
Best Local Similarity	100.0%;	Pred. No. 1e-108;		
Matches 215;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MLACLTVMHLPALNR	TGDPGPGPSTQKTYDITRYLEHQLRSIAGTYLNLGPPFN	60
Db	11	MLACLTVMHLPALNR	TGDPGPGPSTQKTYDITRYLEHQLRSIAGTYLNLGPPFN	70
QY	61	EPDNPFRPGAETPLRATVDLEVMRS	LNDKRLTQNYEAYSHLLCYLRLGRLNQAAATLRL	120
Db	71	EPDNPFRPGAETPLRATVDLEVMRS	LNDKRLTQNYEAYSHLLCYLRLGRLNQAAATLRL	130
QY	121	RSIAHFTCSLQGLGSIAGVMAALGYPLPQPLPGTPTWTTPGPAHSDFLQKMDDFLLKE	180	
Db	131	RSIAHFTCSLQGLGSIAGVMAALGYPLPQPLPGTPTWTTPGPAHSDFLQKMDDFLLKE	190	
QY	181	LQTLWRSKDFNRLKKMKOPPAATAVTLHLGAHGF	215	
Db	191	LQTLWRSKDFNRLKKMKOPPAATAVTLHLGAHGF	225	

Matches 208; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MLACLTCTVWHLPAVPALNRTGDPGPGSIQKTYDLYLTRYLHQLRSLAGTYLNYLGPFPN 60
 Db 11 MLACLTCTVWHLPAVPALNRTGDPGPGSIQKTYDLYLTRYLHQLRSLAGTYLNYLGPFPN 70
 Qy 61 EPDFNPRLGAEATLPRATVNLVWRSNDKRLTONYEAYSHLLCYLRLGNRQAATAELR 120
 Db 71 EPDFNPRLGAEATLPRATVNLVWRSNDKRLTONYEAYSHLLCYLRLGNRQAATAELR 130
 Qy 121 RSLAHFCTSLQGLLGSAGVMAALGYPLPOPLPGCTEPTWTGPAHSDFLQKMDDFWLLKE 180
 Db 131 RSLAHFCTSLQGLLGSAGVMAALGYPLPOPLPGCTEPTWTGPAHSDFLQKMDDFWLLKE 190
 Qy 181 LQTLWRSKDFNRLKKKKMOPPPAAAVTLHLGAHGF 215
 Db 191 LQTLWRSKDFNRLKKKKMOPPPAAAVTLHLGAHGF 225

RESULT 7
 US-09-521-335-2
 ; Sequence 5, Application US/09016534
 ; Patent No. 6143874
 ; GENERAL INFORMATION:
 ; APPLICANT: CHANG, MING-SHI
 ; APPLICANT: ELLIOTT, GARY S.
 ; APPLICANT: SARMIENTO, ULLA
 ; APPLICANT: SENALDI, GIORGIO
 ; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: AMGEN INC.
 ; STREET: ONE AMGEN CENTER
 ; CITY: THOUSAND OAKS
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 91320
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/016.534
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/792,019
 ; FILING DATE: 03-FEB-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: COOK, ROBERT R.
 ; REGISTRATION NUMBER: 31,602
 ; REFERENCE/DOCKET NUMBER: A-442B
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 225 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-016-534-5

Query Match 97.2%; Score 1136; DB 4; Length 225;
 Best Local Similarity 96.7%; Pred. No. 1.1e-118;
 Matches 208; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MLACLTCTVWHLPAVPALNRTGDPGPGSIQKTYDLYLTRYLHQLRSLAGTYLNYLGPFPN 60
 Db 11 MLACLTCTVWHLPAVPALNRTGDPGPGSIQKTYDLYLTRYLHQLRSLAGTYLNYLGPFPN 70
 Qy 61 EPDFNPRLGAEATLPRATVNLVWRSNDKRLTONYEAYSHLLCYLRLGNRQAATAELR 120
 Db 71 EPDFNPRLGAEATLPRATVNLVWRSNDKRLTONYEAYSHLLCYLRLGNRQAATAELR 130

Qy 121 RSLAHFCTSLQGLLGSAGVMAALGYPLPOPLPGCTEPTWTGPAHSDFLQKMDDFWLLKE 180
 Db 131 RSLAHFCTSLQGLLGSAGVMAALGYPLPOPLPGCTEPTWTGPAHSDFLQKMDDFWLLKE 190
 Qy 181 LQTLWRSKDFNRLKKKKMOPPPAAAVTLHLGAHGF 215
 Db 191 LQTLWRSKDFNRLKKKKMOPPPAAAVTLHLGAHGF 225

RESULT 8
 US-09-106-182-3
 ; Sequence 3, Application US/09106182
 ; Patent No. 6046035
 ; GENERAL INFORMATION:
 ; APPLICANT: Shi, Yangu
 ; APPLICANT: Ruben, Steve
 ; TITLE OF INVENTION: Cardiotrophin-Like Cytokine
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc
 ; STREET: 9410 Key West Ave
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: US
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/106,182
 ; FILING DATE: Herewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/051,053
 ; FILING DATE: 30-JUN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Brookes, A. Anders
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PF385
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 301-309-8504
 ; TELEFAX: 301-309-8439
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 203 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-106-182-3

Query Match 10.7%; Score 124.5; DB 3; Length 203;
 Best Local Similarity 28.1%; Pred. No. 5.7e-06;
 Matches 50; Conservative 24; Mismatches 85; Indels 19; Gaps 5;

Qy 30 IQKTYDLYLTRYLHQLRSLAGTYLNYLGPFPNPPNPRLL---GAETLPRATVLDLVWRS 86
 Db 27 IROTHNLARLLTKYADQLLEYVQQGEPFGLPGFSPRLPLAGLSGPPAPSHAGLPV--- 83
 Qy 87 LNDKRLRTQNYEAYSHLLCYLRLGNRQA---TAEIIRSLAHFCTSLQGLLGSAGV 141
 Db 84 ---SERLRQDAALSAIPALLDAVRRRQALNPRAPRLRLSLDEAARQVRAALGAATV 140
 Qy 142 AALGY----PLPOPLPGTEPTWTGPAHSDFLQKMDDFWLLKEIQTWLRSAKDFN 195
 Db 141 AALGAAARGVPPEPV-ATSAFTSNAAGVSAKVLGLHVCGLYGEWVSRTEGDLG 197

RESULT 9
 US-08-233-609-3
 ; Sequence 3, Application US/08233609

STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,534
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442B
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-534-2

Query Match 100.0%; Score 1169; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 2.2e-122;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNLGPPFN 60
DB 11 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNLGPPFN 70
QY 61 EPDFNPRLGAETLPRAVTDLVWRSNDKRLRTQNYEAYSHLLCYLRGLNRQAATAELR 120
DB 71 EPDFNPRLGAETLPRAVTDLVWRSNDKRLRTQNYEAYSHLLCYLRGLNRQAATAELR 130
QY 121 RSLAHFCTSLQGLLSAGTAAAGYPLPQPLPCTEPTWTGPAHSDFLQKMDDFWLKE 180
DB 131 RSLAHFCTSLQGLLSAGTAAAGYPLPQPLPCTEPTWTGPAHSDFLQKMDDFWLKE 190
QY 181 LQTLWRSKDFNRLKKMQPPAAAVTLHLGAHGF 215
DB 191 LQTLWRSKDFNRLKKMQPPAAAVTLHLGAHGF 225

RESULT 5
US-08-792-019B-5
Sequence 5, Application US/08792019B
Patent No. 5741772
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-792-019B-5

Query Match 97.2%; Score 1136; DB 1; Length 225;
Best Local Similarity 96.7%; Pred. No. 1.1e-118;
Matches 208; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNLGPPFN 60
DB 11 MLACLCTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSLAGTYLNLGPPFN 70
QY 61 EPDFNPRLGAETLPRAVTDLVWRSNDKRLRTQNYEAYSHLLCYLRGLNRQAATAELR 120
DB 71 EPDFNPRLGAETLPRAVTDLVWRSNDKRLRTQNYEAYSHLLCYLRGLNRQAATAELR 130
QY 121 RSLAHFCTSLQGLLSAGTAAAGYPLPQPLPCTEPTWTGPAHSDFLQKMDDFWLKE 180
DB 131 RSLAHFCTSLQGLLSAGTAAAGYPLPQPLPCTEPTWTGPAHSDFLQKMDDFWLKE 190
QY 181 LQTLWRSKDFNRLKKMQPPAAAVTLHLGAHGF 215
DB 191 LQTLWRSKDFNRLKKMQPPAAAVTLHLGAHGF 225

RESULT 6
US-08-988-819-5
Sequence 5, Application US/08988819
Patent No. 6054294
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,819
FILING DATE: 12-DEC-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442A
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-988-819-5

Query Match 97.2%; Score 1136; DB 3; Length 225;
Best Local Similarity 96.7%; Pred. No. 1.1e-118;

Db 131 RSLAHFCTSLQGLSGIAGVMAALGYPLPQPLPGTEPTWTGPAHSDFLQKMDDFWLLKE 190
Qy 181 LQTLWRSKDFNRLKKKQPPAAAATVHLGAHGF 215
Db 191 LQTLWRSKDFNRLKKKQPPAAAATVHLGAHGF 225

RESULT 2

US-09-106-182-2
; Sequence 2, Application US/09106182
; Patent No. 6046035
; GENERAL INFORMATION:
; APPLICANT: Shi, Yanggu
; APPLICANT: Ruben, Steve
; TITLE OF INVENTION: Cardiotrophin-Like Cytokine
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc
; STREET: 9410 Key West Ave
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,182
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/051,053
; FILING DATE: 30-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF385
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-106-182-2

Query Match 100.0%; Score 1169; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 2.2e-122;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLACLTIVLWHLPAVPAALNRTGDPGPGSIQKTYDLYLRYLHQLRSLAGTYLNYLGGPPFN 60
Db 11 MLACLTIVLWHLPAVPAALNRTGDPGPGSIQKTYDLYLRYLHQLRSLAGTYLNYLGGPPFN 70
Qy 61 EPDENPRLGAETLPRATVDLEVWRSNDKRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
Db 71 EPDENPRLGAETLPRATVDLEVWRSNDKRLTQNYEAYSHLLCYLRGLNRQAATAELR 130
Qy 121 RSLAHFCTSLQGLSGIAGVMAALGYPLPQPLPGTEPTWTGPAHSDFLQKMDDFWLLKE 180
Db 131 RSLAHFCTSLQGLSGIAGVMAALGYPLPQPLPGTEPTWTGPAHSDFLQKMDDFWLLKE 190
Qy 181 LQTLWRSKDFNRLKKKQPPAAAATVHLGAHGF 215
Db 191 LQTLWRSKDFNRLKKKQPPAAAATVHLGAHGF 225

RESULT 3

US-08-988-819-2

; Sequence 2, Application US/08988819
; Patent No. 6054294
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,819
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442A
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-988-819-2

Query Match 100.0%; Score 1169; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 2.2e-122;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLACLTIVLWHLPAVPAALNRTGDPGPGSIQKTYDLYLRYLHQLRSLAGTYLNYLGGPPFN 60
Db 11 MLACLTIVLWHLPAVPAALNRTGDPGPGSIQKTYDLYLRYLHQLRSLAGTYLNYLGGPPFN 70
Qy 61 EPDENPRLGAETLPRATVDLEVWRSNDKRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
Db 71 EPDENPRLGAETLPRATVDLEVWRSNDKRLTQNYEAYSHLLCYLRGLNRQAATAELR 130
Qy 121 RSLAHFCTSLQGLSGIAGVMAALGYPLPQPLPGTEPTWTGPAHSDFLQKMDDFWLLKE 180
Db 131 RSLAHFCTSLQGLSGIAGVMAALGYPLPQPLPGTEPTWTGPAHSDFLQKMDDFWLLKE 190
Qy 181 LQTLWRSKDFNRLKKKQPPAAAATVHLGAHGF 215
Db 191 LQTLWRSKDFNRLKKKQPPAAAATVHLGAHGF 225

RESULT 4

US-09-016-534-2
; Sequence 2, Application US/09016534
; Patent No. 6143874
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; APPLICANT: ELLIOTT, GARY S.
; APPLICANT: SARMIENTO, ULLA
; APPLICANT: SENALDI, GIORGIO
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER
; CITY: THOUSAND OAKS

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 11:47:42 ; Search time 8.6 Seconds
(without alignments)
735.573 Million cell updates/sec

Title: US-09-521-335-2

Perfect score: 1169

Sequence: 1 MLACLTVMHLPALNRL.....KKMOPPAAVTLHLGAHF 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Minimum number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/prodata/2/iaa/5A COMB.pep.*
- 2: /cgn2_6/prodata/2/iaa/5B COMB.pep.*
- 3: /cgn2_6/prodata/2/iaa/6A COMB.pep.*
- 4: /cgn2_6/prodata/2/iaa/6B COMB.pep.*
- 5: /cgn2_6/prodata/2/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/prodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1169	100.0	225	1	US-08-792-019B-2
2	1169	100.0	225	3	US-09-106-182-2
3	1169	100.0	225	3	US-08-988-819-2
4	1169	100.0	225	4	US-09-016-534-2
5	1136	97.2	225	1	US-08-792-019B-5
6	1136	97.2	225	3	US-08-988-819-5
7	1136	97.2	225	4	US-09-016-534-5
8	124.5	10.7	203	3	US-09-106-182-3
9	118.5	10.1	203	1	US-08-233-609-3
10	118.5	10.1	203	1	US-08-444-083-3
11	118.5	10.1	203	1	US-08-286-304-3
12	118.5	10.1	203	1	US-08-442-745-3
13	118.5	10.1	203	1	US-08-443-129-3
14	118.5	10.1	203	1	US-08-443-952-3
15	118.5	10.1	203	1	US-08-443-130-3
16	118.5	10.1	203	3	US-08-898-911-3
17	118.5	10.1	203	5	PCT-US95-04467-3
18	91.5	7.8	201	1	US-08-444-083-8
19	91.5	7.8	201	1	US-08-286-304-8
20	91.5	7.8	201	1	US-08-442-745-8
21	91.5	7.8	201	1	US-08-443-129-8
22	91.5	7.8	201	1	US-08-443-952-8
23	91.5	7.8	201	1	US-08-443-130-8
24	91.5	7.8	201	1	US-08-792-019B-11
25	91.5	7.8	201	3	US-09-106-182-4
26	91.5	7.8	201	3	US-08-988-819-11
27	91.5	7.8	201	3	US-08-898-911-8

28	91.5	7.8	201	4	US-09-016-534-11	Sequence 11, Appl
29	91.5	7.8	201	5	PCT-US95-04467-8	Sequence 8, Appl
30	91	7.8	195	1	US-07-959-284-5	Sequence 5, Appl
31	91	7.8	195	2	US-08-308-736A-5	Sequence 5, Appl
32	91	7.8	195	4	US-08-645-107A-5	Sequence 5, Appl
33	91	7.8	195	4	US-09-197-349-5	Sequence 5, Appl
34	91	7.8	195	5	PCT-US92-08258-2	Sequence 2, Appl
35	91	7.8	195	5	PCT-US93-09649A-5	Sequence 5, Appl
36	91	7.8	195	5	PCT-US93-09649-5	Sequence 5, Appl
37	91	7.8	1182	4	US-09-287-354-6	Sequence 6, Appl
38	87.5	7.5	1207	4	US-09-287-354-5	Sequence 5, Appl
39	85.5	7.3	560	2	US-08-756-317-11	Sequence 11, Appl
40	84	7.2	200	4	US-08-949-155-4	Sequence 4, Appl
41	84	7.2	200	4	US-09-819-964-4	Sequence 4, Appl
42	82	7.0	200	1	US-07-959-284-8	Sequence 8, Appl
43	82	7.0	200	2	US-08-308-736A-8	Sequence 8, Appl
44	82	7.0	200	4	US-08-645-107A-8	Sequence 8, Appl
45	82	7.0	200	4	US-09-197-349-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-792-019B-2
; Sequence 2, Application US/08792019B
; Patent No. 5741772
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: THE NEUTROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DEHAVILLAND DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,019B
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 225 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-792-019B-2

Query Match 100.0%; Score 1169; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 2.2e-122;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MLACLTVMHLPALNRLTGDGPGPSIQKTYDTRYLHQLRSLAGTYLNLVLPPEP	60
DB	11	MLACLTVMHLPALNRLTGDGPGPSIQKTYDTRYLHQLRSLAGTYLNLVLPPEP	70
QY	61	EPDFNPRLCAETLPATVDLVWRSLNDKRLRTQNYEAYSHLLCYLRLGNRQAATAE	120
DB	71	EPDFNPRLCAETLPATVDLVWRSLNDKRLRTQNYEAYSHLLCYLRLGNRQAATAE	130
QY	121	RSIAHFTCSLQGLSGIAGVMAALGYPLPPLPGTPTWTTPGPAHSDFLOKMDFFWL	180

Query Match 97.2%; Score 1136; DB 19; Length 225;
Best Local Similarity 96.7%; Pred. No. 1.5e-111;
Matches 208; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MLACLTVLWHLPAVPALNRTGDPGPGPSIOKTYDLTRYLEHQLRSLAGTYLNYLGPFPN 60
Db 11 MLACLTVLWHLPAVPALNRTGDPGPGPSIOKTYDLTRYLEHQLRSLAGTYLNYLGPFPN 70

Qy 61 EPDFNPRLGAETLPRATVDLEVWRSNDKRLRLTONYEAYSHLLCYLRGLNRQAATAELR 120
Db 71 EPDFNPRLGAETLPRATVNLVWRSNDRLRLTONYEAYSHLLCYLRGLNRQAATAELR 130

Qy 121 RSLAHFCTSLQGLLSIAGVMAALGYPLQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
Db 131 RSLAHFCTSLQGLLSIAGVMAALGYPLQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 190

Qy 181 LQTLWRSKADFNRLKKMQPPAAAVTLHLGAHGF 215
Db 191 LQTLWRSKADFNRLKKMQPPAAASVTLHLEAHGF 225

Search completed: March 13, 2003, 11:49:17
Job time : 23.704 secs

LT 15
6142
ID AAW56142 standard; Protein; 225 AA.
XX
AC AAW56142;
XX
DT 13-JUL-1998 (first entry)
XX
DE Amino acid sequence of murine neurotrophic factor NNT-1.
XX
KW Mouse; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;
XX treatment; neurological disease; degeneration; Parkinson's disease;
KW amyotrophic lateral sclerosis; ALS; Alzheimers's disease; stroke.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..27
FT Protein /note= "signal peptide"
FT /note= "mature peptide"
XX
PN US5741772-A.
XX
PD 21-APR-1998.
XX
PF 03-FEB-1997; 97US-0792019.
XX
03-FEB-1997; 97US-0792019.
XX
PA (AMGE-) AMGEN INC.
XX
PI Chang M;
XX
DR WPI; 1998-260526/23.
DR N-PSDB; AAV22654.
XX
PT Neurotrophic factor NNT-1 polypeptide and related nucleic acids -
PT useful for stimulating growth of motor and sympathetic neurons
XX
PS Claim 2; Fig 5; 41pp; English.
XX
CC The present sequence represents a murine neurotrophic factor, designated
CC NNT-1, which is capable of stimulating growth of motor or sympathetic
CC neurons. The NNT-1 protein is useful in the treatment of neurological
CC diseases characterised by the degeneration and death of particular
CC classes of neurons. These diseases specifically include Parkinson's
CC disease, amyotrophic lateral sclerosis (ALS), Alzheimers's disease,
CC stroke and various degenerative disorders affecting vision.
XX
SQ Sequence 225 AA;

XX Mouse interleukin-B60 (IL-B60).

XX Interleukin-B60; IL-B60; mouse; cytokine; cytokine-like factor-1;

KW haematopoietic; inflammation; antiinflammatory; autoimmune disease;

KW therapy.

XX Mus musculus.

OS

XX Key Location/Qualifiers

FT Peptide 1..17

FT Protein /label= Signal_peptide

FT /label= Mature-protein

XX WO200053631-A1.

XX 14-SEP-2000.

XX 09-MAR-2000; 2000WO-US06182.

XX 11-MAR-1999; 99US-0267901.

XX (SCHE) SCHERING CORP.

PA Oppmann B, Timans JC; Kastelein RA, Bazan JF;

PI WPI: 2000-587426/55.

XX N-PSDB; AAA88547.

XX Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,

PT polypeptides, and nucleic acids, useful in research, diagnosis and for

PT treating inflammatory and autoimmune disorders -

XX Claim 1; Page 17; 97pp; English.

XX The present sequence is that of mouse interleukin-B60 (IL-B60), a

CC novel, small soluble cytokine-like protein that exhibits structural

CC motifs characteristic of a member of the long-chain cytokines, and

CC which shows homology to granulocyte colony stimulating factor and

CC interleukin-6. IL-6B0 may have either stimulatory or inhibitory

CC effects on haematopoietic cells, including e.g. lymphoid cells,

CC such as T-cells, B-cells, natural killer cells, macrophages,

CC dendritic cells, haematopoietic progenitors, etc. Methods are

CC provided for modulating the physiology or development of a cell or

CC tissue culture cells by contacting the cell with an agonist or

CC antagonist of IL-B60 or an agonist of antagonist of a complex of

CC mature IL-B60 and its partner, cytokine-like factor-1 (CLF-1, see

CC AAB19588). The IL-B60/CLF-1 cytokine serves as a key physiological

CC factor in motor neuron development and regeneration. IL-60B, its

CC agonists and antagonists may be used to treat inflammatory or

CC autoimmune disorders and also for drug screening.

XX Query Match 97.2%; Score 1136; DB 21; Length 215;

XX Best Local Similarity 96.7%; Pred. No. 1.4e-111;

XX Matches 208; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MLACLCVTLMHLPVAPALNRTGDPGPGPSIQKTYDLYRLEHQLRSAGTYLNYLGPPFN 60

DB 1 MLACLCVTLMHLPVAPALNRTGDPGPGPSIQKTYDLYRLEHQLRSAGTYLNYLGPPFN 60

QY 61 EPDPNPRLGAEITPRATVDLEVRSLNDKRLRTQNYEAYSHLLCYLRGLNRQATAEELR 120

DB 61 EPDPNPRLGAEITPRATVNLVWRSLNDKRLRTQNYEAYSHLLCYLRGLNRQATAEELR 120

QY 121 RSLAHFCTSLQGLLGSAGVMAALGYLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180

DB 121 RSLAHFCTSLQGLLGSAGVMAALGYLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180

QY 181 LQTLWRSKDFNRLKKMQPPAASVTLHLGAHGF 215

Db 181 LQTLWRSKDFNRLKKMQPPAASVTLHLGAHGF 215

RESULT 14

AAW29716

ID AAW29716 standard; Protein; 225 AA.

XX AAW29716;

AC AAW29716;

XX 09-NOV-1998 (first entry)

DT Mouse neurotrophic factor NNT-1.

XX

DE NNT-1; neurotrophic factor; mouse; antiinflammatory; adjuvant;

XX Alzheimer's disease; Parkinson's disease; Huntington's disease;

KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;

KW peripheral neuropathy; dystrophy; neural retina degeneration;

KW common variable immunodeficiency; CVID; selective IgA deficiency;

KW hypogammaglobulinaemia; X-linked agammaglobulinaemia; antiseptic;

KW therapy.

XX Mus sp.

XX Key Location/Qualifiers

FT Peptide 1..27

FT Protein /label= Sig_peptide

FT /label= Mat_protein

XX WO9833922-A1.

XX 05-AUG-1998.

XX 02-FEB-1998; 98WO-US02363.

XX 30-JAN-1998; 98US-0016534.

PR 03-FEB-1997; 97US-0792019.

XX (AMGE-) AMGEN INC.

XX Chang M, Elliot GS, Sarmiento U, Senaldi G;

XX WPI: 1998-437475/37.

DR N-PSDB; AAV47512.

XX Newly isolated nucleic acid encoding human or murine neurotrophic

PT factor NNT-1 - useful for treatment of neurological and

PT immunological diseases or inflammation, also as vaccine adjuvant

XX Claim 13; Fig 5; 120pp; English.

XX This is the amino acid sequence of a murine neurotrophic factor,

CC designated NNT-1, that is a growth factor for neurons and for B or

CC T cells. It was deduced from isolated NNT-1 cDNA (see AAV47512).

CC Human NNT-1 (see AAW29715) is also provided. Vectors and host cells

CC for use in the production of human murine recombinant NNT-1

CC polypeptides. These are used to treat: (i) neurological or

CC immunological diseases, specifically Alzheimer's, Parkinson's

CC or Huntington's diseases, amyotrophic lateral sclerosis,

CC Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and

CC degeneration of the neural retina, or conditions characterised by T

CC or B cell defects, e.g. common variable immunodeficiency (CVID),

CC selective IgA deficiency, hypogammaglobulinaemia and X-linked

CC agammaglobulinaemia (claimed), but many others disclosed; and (ii)

CC inflammation. NNT-1 is also able to boost immunoreactivity and

CC antibody production following vaccination, and, since it inhibits

CC tumour necrosis factor production, it may also be useful for

CC treating sepsis. In addition, cells that have been engineered to

CC express NNT-1 can be implanted, or nucleic acids are delivered in

CC gene therapy vectors.

XX Sequence 225 AA;

XX 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX WPI; 2001-476283/51.
DR N-PSDB; AAK51548.
XX Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
PS Claim 20; Page 3306; 6221pp; English.
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX SQ Sequence 260 AA;
Query Match 99.4%; Score 1162; DB 22; Length 260;
Best Local Similarity 99.5%; Pred. No. 3.3e-114;
Matches 214; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MLACLTVLWHLPAVPALNRTGDPGPGSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
Db 46 MLACLTVLWHLPAVPALNRTGDPGPGSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 105
61 EPDFNPRLGAETLPRAVDLEWVRSNDKRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
Db 106 EPDFNPRLGAETLPRAVDLEWVRSNDKRLTQNYEAYSHLLCYLRGLNRQAATAELR 165
Qy 121 RSLAHFCTSLOGLLSAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
Db 166 RSLAHFCTSLOGLLSAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 225
Qy 181 LQTLWRSKDFNRLKKKQPPAAAATVHLGAHF 215
Db 226 LQTLWRSKDFNRLKKKQPPAAAATVHLGAHF 260
RESULT 12
AAE00828
XX AAE00828 standard; Protein; 223 AA.
XX AAE00828;
DT 02-JUL-2001 (first entry)
XX Human cardiotrophin-like cytokine (CLC) protein.
DE Human; biologically active complex; haemopoietin receptor; NR6;
XX Human; biologically active complex; haemopoietin receptor; NR6;
KW

KW cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation;
KW differentiation; cell survival; neurotrophic activity.
OS Homo sapiens.
XX Key Location/Qualifiers
FT Peptide 1..27 /label= signal_peptide
FT Protein 28..223 /label= Human mature CLC protein
FT /note= "Cardiotrophin-like cytokine"
XX WO200127157-A1.
PN 19-APR-2001.
XX 06-OCT-2000; 2000WO-AU01216.
XX 08-OCT-1999; 99AU-0003327.
PR 12-MAY-2000; 2000AU-0007489.
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX Nash A, Jachno KM, Fabri LJ, Reid K, Bartlett PF, Hilton DJ;
PI Nakata Y, Hasegawa M;
XX WPI; 2001-281978/29.
DR N-PSDB; AAD04201.
XX New biologically active complex comprising NR6 and
FT cardiotrophin-like-cytokine, for facilitating proliferation,
PT differentiation and/or survival of a cell -
XX Claim 32; Page 114-115; 123pp; English.
XX The present invention relates to a biologically active complex comprising
CC a haemopoietin receptor, NR6 and cardiotrophin-like cytokine (CLC).
CC The complex is useful in the manufacture of a medicament for the
CC treatment and/or prophylaxis of a subject, as it is involved in
CC facilitating proliferation, differentiation and/or survival of a cell.
CC The complex or its components have neurotrophic activity. The present
CC sequence is human cardiotrophin-like cytokine (CLC) protein.
XX SQ Sequence 223 AA;
Query Match 99.0%; Score 1157; DB 22; Length 223;
Best Local Similarity 100.0%; Pred. No. 9.1e-114;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MLACLTVLWHLPAVPALNRTGDPGPGSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
Db 11 MLACLTVLWHLPAVPALNRTGDPGPGSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 70
Qy 61 EPDFNPRLGAETLPRAVDLEWVRSNDKRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
Db 71 EPDFNPRLGAETLPRAVDLEWVRSNDKRLTQNYEAYSHLLCYLRGLNRQAATAELR 130
Qy 121 RSLAHFCTSLOGLLSAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
Db 131 RSLAHFCTSLOGLLSAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 190
Qy 181 LQTLWRSKDFNRLKKKQPPAAAATVHLGAH 213
Db 191 LQTLWRSKDFNRLKKKQPPAAAATVHLGAH 223
RESULT 13
AAE19587
ID AAE19587 standard; Protein; 215 AA.
XX AAE19587;
DT 22-JAN-2001 (first entry)

CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a novel human
CC polypeptide of the invention.
XX
SQ Sequence 321 AA;
Query Match 100.0%; Score 1169; DB 22; Length 321;
Best Local Similarity 100.0%; Pred. No. 8.1e-115;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLACLTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQHRSAGTYLVNLGPPFN 60
DB 107 MLACLTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQHRSAGTYLVNLGPPFN 166
QY 61 EPDFNPRLGAETLPRAVDLEVWRSNDKRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
DB 167 EPDFNPRLGAETLPRAVDLEVWRSNDKRLTQNYEAYSHLLCYLRGLNRQAATAELR 226
QY 121 RSLAHFCTSLQGLLSIAGVMAALGYPLPQLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
DB 227 RSLAHFCTSLQGLLSIAGVMAALGYPLPQLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 286
QY 181 LQTLWRSKDFNRLKKMQPPAAAVTLHLGAHGF 215
DB 287 LQTLWRSKDFNRLKKMQPPAAAVTLHLGAHGF 321
RESULT 10
AAM79399
ID AAM79399 standard; Protein; 321 AA.
XX
AC AAM79399;
XX
DT 06-NOV-2001 (first entry)
L Human protein SEQ ID NO 3045.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US04098.
XX 03-FEB-2000; 2000US-0496914.
XX 27-APR-2000; 2000US-0560875.
XX 20-JUN-2000; 2000US-0598075.
XX 19-JUL-2000; 2000US-0620325.
XX 01-SEP-2000; 2000US-0654936.
XX 15-SEP-2000; 2000US-0663561.
XX 20-OCT-2000; 2000US-0693325.
XX 30-NOV-2000; 2000US-0728422.
XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX WPI; 2001-476283/51.
DR N-PSDB; AAK52532.
XX Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX Claim 20; Page 237; 5221pp; English.
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation of which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 321 AA;
Query Match 100.0%; Score 1169; DB 22; Length 321;
Best Local Similarity 100.0%; Pred. No. 8.1e-115;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLACLTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQHRSAGTYLVNLGPPFN 60
DB 107 MLACLTVLWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQHRSAGTYLVNLGPPFN 166
QY 61 EPDFNPRLGAETLPRAVDLEVWRSNDKRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
DB 167 EPDFNPRLGAETLPRAVDLEVWRSNDKRLTQNYEAYSHLLCYLRGLNRQAATAELR 226
QY 121 RSLAHFCTSLQGLLSIAGVMAALGYPLPQLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
DB 227 RSLAHFCTSLQGLLSIAGVMAALGYPLPQLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 286
QY 181 LQTLWRSKDFNRLKKMQPPAAAVTLHLGAHGF 215
DB 287 LQTLWRSKDFNRLKKMQPPAAAVTLHLGAHGF 321
RESULT 11
AAM78415
ID AAM78415 standard; Protein; 260 AA.
XX
AC AAM78415;
XX
DT 06-NOV-2001 (first entry)
L Human protein SEQ ID NO 1077.
XX
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US04098.

KW antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder.
XX
XX
OS Homo sapiens.
XX
XX WO200153455-A2.
XX
XX 26-JUL-2001.
XX
XX 22-DEC-2000; 2000WO-US35017.
XX
XX 23-DEC-1999; 99US-0471275.
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-457603/49.
DR N-PSDB; AAH99772.
XX
XX Isolated human polynucleotides encoding polypeptides, useful for the
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
XX
XX Claim 20; Page 278; 1217pp; English.
XX
XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC AAM25963. The proteins can have activities based on the tissues and
CC cells they are expressed in, such as: antiinflammatory; antirheumatic;
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant;
CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC cardiovascular; antianaemic; antiaggregant; haemostatic; vulnery;
CC antitumor; osteopathic; dermatological; antiallergic; antiasthmatic;
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders.
XX
SQ Sequence 253 AA;
Query Match 100.0%; Score 1169; DB 22; Length 253;
Best Local Similarity 100.0%; Pred. No. 5.8e-115; Mismatches 0; Gaps 0;
Matches 215; Conservative 0; Indels 0;
QY 1 MLACLCTVLWHLPVAPALNRTGDPGPGPSIQKTYDILTRYLEHQLRSLAGTYLNYLGGPPN 60
DB 39 MLACLCTVLWHLPVAPALNRTGDPGPGPSIQKTYDILTRYLEHQLRSLAGTYLNYLGGPPN 98
QY 61 EPDFNPPRLGAEATLPRATVDLEWRSNLDKRLTQNYEAYSHLLCYLRGLNQAATAELR 120
DB 99 EPDFNPPRLGAEATLPRATVDLEWRSNLDKRLTQNYEAYSHLLCYLRGLNQAATAELR 158
QY 121 RSLAHECTSLQGLGSIAGVMAALGYPLPQPLPGTEPTTPGPAHSDFLQKDDFWLLKE 180
DB 159 RSLAHECTSLQGLGSIAGVMAALGYPLPQPLPGTEPTTPGPAHSDFLQKDDFWLLKE 218
QY 181 LQTWLRSAKDFNRLKKMQPPAAAATLHLGAHGF 215

DB 219 LQTWLRSAKDFNRLKKMQPPAAAATLHLGAHGF 253
RESULT 9
ABB11896
ID ABB11896 standard; peptide; 321 AA.
XX
XX ABB11896;
XX
XX 11-JAN-2002 (first entry)
XX
XX Human cardiotrophin-like cytokine homologue, SEQ ID NO:2266.
XX
XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibitor; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnery; antitumor.
XX
XX Homo sapiens.
OS
XX WO200157188-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001WO-US03800.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-457740/49.
DR N-PSDB; ABA09140.
XX
XX Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
PT e.g. arthritis and cancer -
XX
XX Claim 20; Page 273; 1963pp; English.
XX
XX Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities, stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell

CC inhibit differentiation of cells stocks. The complex is also used to
CC modulate activity of the gp130/IL6 receptor or cells expressing
CC that receptor, particularly those cells implicated in the immune,
CC haematopoietic, nervous or reproductive system, the liver or skeletal
CC muscle. Molecules of the invention may be used to prevent or treat
CC neurodegenerative diseases, including anyotropic lateral sclerosis,
CC Parkinson's and Huntington's disease, to repair or regenerate nervous
CC or muscular tissue or to maintain muscular mass in paralysis patients.
CC They may also be used to treat cancer, obesity and associated diseases,
CC and to improve fertility, particularly to avoid endometriosis and/or
CC assist blastocyst implantation, thrombosis, or retinal disease,
CC particular retinal pigmentosis.

XX
SQ Sequence 225 AA;
Query Match 100.0%; Score 1169; DB 22; Length 225;
Best Local Similarity 100.0%; Pred. No. 5e-115;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MLACLTVLWHLPAVPALNRTGDPGPGSIQKTYDLYLRYLHQLRSLAGTYLNLGPPFN 60
Db 11 MLACLTVLWHLPAVPALNRTGDPGPGSIQKTYDLYLRYLHQLRSLAGTYLNLGPPFN 70

QY 61 EPDFNPRLGAETLPRAATVLEWRSNDKRLTQNTYEAISHLLCYLRGLNRQAATAELR 120
Db 71 EPDFNPRLGAETLPRAATVLEWRSNDKRLTQNTYEAISHLLCYLRGLNRQAATAELR 130

QY 121 RSLAHFCTSLQGLGSIAGVMAALGYPLPQPLGCTEPTTTPGPAHSDFLQKMDDFWLLKE 180
Db 131 RSLAHFCTSLQGLGSIAGVMAALGYPLPQPLGCTEPTTTPGPAHSDFLQKMDDFWLLKE 190

QY 181 LQTLWRSKDFNRLKKMKQPPAAAATLHLGAHGF 215
Db 191 LQTLWRSKDFNRLKKMKQPPAAAATLHLGAHGF 225

RESULT 7
ID AAU78176
AAU78176 standard; Protein; 225 AA.

AC AAU78176;
XX
XX 05-JUN-2002 (first entry)
XX Human novel neurotrophic factor NNT1.

XX Human; NNT1; neurotrophic factor; IgE-related disease;
XX type I allergic disease; allergic rhinitis; eczema; dermatitis;
XX pollinosis; asthma; immune disease; cancer; arteriosclerosis;
XX vascular restenosis; rheumatoid arthritis; psoriatic arthritis;
XX inflammatory arthritis; osteoarthritis; inflammatory joint disease;
XX autoimmune disease; multiple sclerosis; lupus; diabetes; endometriosis;
XX inflammatory bowel disease; transplant rejection; reproductive disorder;
XX graft versus host disease; infertility; miscarriage; preterm labour.

XX Homo sapiens.
XX
XX OS
XX WO200215977-A2.
XX
XX 28-FEB-2002.
XX
XX 17-AUG-2001; 2001WO-US25906.
XX
XX 18-AUG-2000; 2000US-226436P.
XX
XX 16-AUG-2001; 2001US-0931704.
XX
XX (AMGE-) AMGEN INC.
XX
XX Senaldi G;
XX
XX WPI; 2002-280867/32.
XX
XX N-PSDB; ABK11647.

PT Treating Immunoglobulin E-related disease, modulating IgE levels in a
PT patient, preventing IgE-related disease and treating allergic diseases,
PT involves administering NNT-1 inhibitor to a patient
XX
PS Claim 2; Fig 3; 63pp; English.

XX The invention relates to treating Immunoglobulin E (IgE)-related disease,
CC modulating IgE levels in a patient, preventing an IgE-related disease,
CC and treating allergic diseases, comprising administering a
CC therapeutically effective amount of novel neurotrophic factor (NNT)-1
CC inhibitor to a patient. Also included are a method of diagnosing an
CC IgE-related disease or susceptibility to an IgE-related disease, by
CC determining the presence or amount of expression of an NNT1 polypeptide
CC encoded by a NNT1 nucleotide sequence, its fragment or naturally
CC occurring variant, and diagnosing an IgE-related disease or
CC susceptibility of an IgE-related disease based on the presence or amount
CC of expression of the polypeptide and a pharmaceutical composition for use
CC in treating IgE-related disease, comprising the NNT1 inhibitor.

CC The NNT1 inhibitor is useful for preventing and treating IgE-related
CC disease, modulating IgE levels, and treating allergic diseases e.g.
CC type I allergic disease, allergic rhinitis, eczema, dermatitis,
CC pollinosis, asthma, immune diseases and disorders, diseases involving
CC abnormal cell proliferation including cancer, arteriosclerosis and
CC vascular restenosis, diseases and conditions relating to dysfunction of
CC immune system including rheumatoid arthritis, psoriatic arthritis,
CC inflammatory arthritis, osteoarthritis, inflammatory joint disease,
CC autoimmune disease, multiple sclerosis, lupus, diabetes, inflammatory
CC bowel disease, transplant rejection, and graft versus host disease, and
CC reproductive diseases and disorders including infertility, miscarriage,
CC preterm labour and delivery, and endometriosis. The present sequence
CC represents human NNT1.

XX
SQ Sequence 225 AA;
Query Match 100.0%; Score 1169; DB 23; Length 225;
Best Local Similarity 100.0%; Pred. No. 5e-115;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLACLTVLWHLPAVPALNRTGDPGPGSIQKTYDLYLRYLHQLRSLAGTYLNLGPPFN 60
Db 11 MLACLTVLWHLPAVPALNRTGDPGPGSIQKTYDLYLRYLHQLRSLAGTYLNLGPPFN 70

QY 61 EPDFNPRLGAETLPRAATVLEWRSNDKRLTQNTYEAISHLLCYLRGLNRQAATAELR 120
Db 71 EPDFNPRLGAETLPRAATVLEWRSNDKRLTQNTYEAISHLLCYLRGLNRQAATAELR 130

QY 121 RSLAHFCTSLQGLGSIAGVMAALGYPLPQPLGCTEPTTTPGPAHSDFLQKMDDFWLLKE 180
Db 131 RSLAHFCTSLQGLGSIAGVMAALGYPLPQPLGCTEPTTTPGPAHSDFLQKMDDFWLLKE 190

QY 181 LQTLWRSKDFNRLKKMKQPPAAAATLHLGAHGF 215
Db 191 LQTLWRSKDFNRLKKMKQPPAAAATLHLGAHGF 225

RESULT 8
ID AAM25831
AAM25831 standard; Protein; 253 AA.

XX
XX AAM25831;
XX
XX 16-OCT-2001 (first entry)
XX
XX Human protein sequence SEQ ID NO:1346.

XX Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
XX antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;
XX antibacterial; endocrine; cardiant; central nervous system; virucide;
XX anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;
XX antiaggregant; haemostatic; vulnery; antitumor; osteopathic; eczema;
XX dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;
XX neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;
XX immunostimulant; gene therapy; antitense therapy; vaccine; inflammation;

XX 13-JUL-1998 (first entry)
XX Amino acid sequence of human neurotrophic factor NNT-1.
XX Human; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;
KW treatment; neurological disease; degeneration; Parkinson's disease;
KW amyotrophic lateral sclerosis; ALS; Alzheimer's disease; stroke.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..27 /note= "signal peptide"
FT Protein 28..225 /note= "mature protein"
FT US5741772-A.
XX 21-APR-1998.
XX 03-FEB-1997; 97US-0792019.
XX 03-FEB-1997; 97US-0792019.
XX (AMGE-) AMGEN INC.
XX Chang M;
XX WPI; 1998-260526/23.
XX N-PSDB; AAV22652.
XX Neurotrophic factor NNT-1 polypeptide and related nucleic acids -
PT useful for stimulating growth of motor and sympathetic neurons
XX Claim 1; Fig 3; 41pp; English.
XX The present sequence represents a human neurotrophic factor, designated
CC NNT-1, which is capable of stimulating growth of motor or sympathetic
CC neurons. The NNT-1 protein is useful in the treatment of neurological
CC diseases characterised by the degeneration and death of particular
CC classes of neurons. These diseases specifically include Parkinson's
CC disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,
CC stroke and various degenerative disorders affecting vision.
XX Sequence 225 AA;
Query Match 100.0%; Score 1169; DB 19; Length 225;
Best Local Similarity 100.0%; Pred. No. 5e-115;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLACLCVTLMWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSAGTYLNYLGPFFN 60
Db 11 MLACLCVTLMWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSAGTYLNYLGPFFN 70
QY 61 EPDFNPRLGAETLPRAVTDLVWRSINDKRLTONVEAYSHLLCYLRGLNRQATAELR 120
Db 71 EPDFNPRLGAETLPRAVTDLVWRSINDKRLTONVEAYSHLLCYLRGLNRQATAELR 130
QY 121 RSLAHFCTSLQGLSGIAGVMAALGYPLPQLPCTEPTTTPGPAHSDFLQKMDDFWLLKE 180
Db 131 RSLAHFCTSLQGLSGIAGVMAALGYPLPQLPCTEPTTTPGPAHSDFLQKMDDFWLLKE 190
QY 181 LQTLWRSKDFNRLKKMQPPAAAVTLHLGAHGF 215
Db 191 LQTLWRSKDFNRLKKMQPPAAAVTLHLGAHGF 225
RESULT 4
AAW94466
ID AAW94466 standard; Protein; 225 AA.
XX
AC AAW94466;

XX 22-APR-1999 (first entry)
XX Human cardiotrophin-like cytokine protein.
XX Human; cardiotrophin-like cytokine; interleukin 6 cytokine family;
KW CLC; IL-6; diagnosis; detection; immune system-related disorder;
KW cancer; cardiac disorder; heart failure; hypertension; cancer;
KW autoimmune disorder; infection.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..27 /label= signal
FT Protein 28..225 /label= Cardiotrophin-like_cytokine
FT Domain 74..79 /label= CD-I
FT /note= "conserved domain"
FT Domain 150..156 /label= CD-II
FT /note= "conserved domain"
FT Domain 194..198 /label= CD-III
FT /note= "conserved domain"
XX WO9900415-A1.
XX 07-JAN-1999.
XX 29-JUN-1998; 98WO-US13129.
XX 30-JUN-1997; 97US-0051311.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Shi Y;
PI WPI; 1999-095678/08.
DR N-PSDB; AAX16161.
XX New isolated cardiotrophin-like cytokine nucleic acid - used to
PT develop products for treating cardiac and immune system disorders,
PT e.g. heart failure, hypertension, cancers, autoimmune disorders and
PT infections
XX Claim 1; Fig 1; 103pp; English.
XX The present invention relates to a novel cardiotrophin-like cytokine
CC (CLC) protein which is a member of the interleukin 6 (IL-6) cytokine
CC family. The present sequence represents the human CLC protein. The
CC present invention also describes screening methods for identifying
CC agonists and antagonists of CLC activity, as well as methods for
CC detecting cardiac and immune system-related disorders and
CC therapeutic methods for treating cardiac and immune system-related
CC disorders, e.g. heart failure, hypertension, cancers, autoimmune
CC disorders and infections.
XX Sequence 225 AA;
Query Match 100.0%; Score 1169; DB 20; Length 225;
Best Local Similarity 100.0%; Pred. No. 5e-115;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLACLCVTLMWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSAGTYLNYLGPFFN 60
Db 11 MLACLCVTLMWHLPAVPALNRTGDPGPGPSIQKTYDLTRYLEHQLRSAGTYLNYLGPFFN 70
QY 61 EPDFNPRLGAETLPRAVTDLVWRSINDKRLTONVEAYSHLLCYLRGLNRQATAELR 120
Db 71 EPDFNPRLGAETLPRAVTDLVWRSINDKRLTONVEAYSHLLCYLRGLNRQATAELR 130

XX WPI; 2000-587426/55.
DR N-PSDB; AAA88546.
XX Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,
PT polypeptides, and nucleic acids, useful in research, diagnosis and for
PT treating inflammatory and autoimmune disorders -
XX Claim 1; Page 15-16; 97pp; English.
XX The present sequence is that of human interleukin-B60 (IL-B60), a
CC novel, small soluble cytokine-like protein that exhibits structural
CC motifs characteristic of a member of the long-chain cytokines, and
CC which shows homology to granulocyte colony stimulating factor and
CC interleukin-6. IL-60B may have either stimulatory or inhibitory
CC effects on haematopoietic cells, including e.g. lymphoid cells,
CC such as T-cells, B-cells, natural killer cells, macrophages,
CC dendritic cells, haematopoietic progenitors, etc. Methods are
CC provided for modulating the physiology or development of a cell or
CC tissue culture cells by contacting the cell with an agonist or
CC antagonist of IL-B60 or an agonist of antagonist of a complex of
CC mature IL-B60 and its partner, cytokine-like factor-1 (CLF-1, see
CC AAB19588). The IL-B60/CLF-1 cytokine serves as a key physiological
CC factor in motor neuron development and regeneration. IL-60B, its
CC agonists and antagonists may be used to treat inflammatory or
CC autoimmune disorders and also for drug screening.

SQ Sequence 215 AA;

Query Match 100.0%; Score 1169; DB 21; Length 215;
Best Local Similarity 100.0%; Pred. No. 4.7e-115;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MLACLCVTLVHLPVAPALNRTGDPGPGSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
Db 1 MLACLCVTLVHLPVAPALNRTGDPGPGSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
Oy 61 EPDFNPRLGAETLPRAVTDLEWVRSNDKRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
Db 61 EPDFNPRLGAETLPRAVTDLEWVRSNDKRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
Oy 121 RSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
Db 121 RSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
Oy 181 LQTLWRSKADFNRLKKMQPPAAAVTLHLGAHGF 215
Db 181 LQTLWRSKADFNRLKKMQPPAAAVTLHLGAHGF 215

RESULT 2
AAW29715
ID AAW29715 standard; Protein; 225 AA.
XX AAW29715;
AC AAW29715;
DT 09-NOV-1998 (first entry)
XX Human neurotrophic factor NNT-1.
DE NNT-1; neurotrophic factor; human; antiinflammatory; adjuvant;
XX Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
KW peripheral neuropathy; dystrophy; neural retina degeneration;
KW common variable immunodeficiency; CVID; selective IGA deficiency;
KW hypogammaglobulinaemia; X-linked agammaglobulinaemia; antiseptic;
KW therapy.

OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Peptide 1..27
FT /label= Sig_peptide

FT Protein 28..225
XX /label= Mat_protein
FN WO9833922-A1.
PD 06-AUG-1998.
XX 02-FEB-1998; 98WO-US02363.
PF 30-JAN-1998; 98US-0016534.
XX 03-FEB-1997; 97US-0792019.
PR (AMGE-) AMGEN INC.
XX Chang M, Elliot GS, Sarmiento U, Senaldi G;
XX WPI; 1998-437475/37.
XX N-PSDB; AAV47510-11.
XX Newly isolated nucleic acid encoding human or murine neurotrophic
PT factor NNT-1 - useful for treatment of neurological and
PT immunological diseases or inflammation, also as vaccine adjuvant
XX Claim 12; Fig 3; 120pp; English.

This is the amino acid sequence of a novel neurotrophic factor,
designated NNT-1, that is a growth factor for neurons and for B or
T cells. It was deduced from isolated cDNA (see AAV47510) and
genomic DNA (see AAV47511) clones. Vectors containing the cDNA or
genomic DNA and host cells are provided for use in the production
of NNT-1 polypeptides. These are used to treat: (i) neurological
or immunological diseases, specifically Alzheimer's, Parkinson's
or Huntington's disease, amyotrophic lateral sclerosis,
Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and
degeneration of the neural retina, or conditions characterised by T
or B cell defects, e.g. common variable immunodeficiency (CVID),
selective IGA deficiency, hypogammaglobulinaemia and X-linked
agammaglobulinaemia (claimed), but many others disclosed; and (ii)
inflammation. NNT-1 is also able to boost immunoreactivity and
antibody production following vaccination, and, since it inhibits
tumour necrosis factor production, it may also be useful for
treating sepsis. In addition, cells that have been engineered to
express NNT-1 can be implanted, or nucleic acids are delivered in
gene therapy vectors.

SQ Sequence 225 AA;

Query Match 100.0%; Score 1169; DB 19; Length 225;
Best Local Similarity 100.0%; Pred. No. 5e-115;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MLACLCVTLVHLPVAPALNRTGDPGPGSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 60
Db 11 MLACLCVTLVHLPVAPALNRTGDPGPGSIQKTYDLTRYLEHQLRSLAGTYLNYLGPPFN 70
Oy 61 EPDFNPRLGAETLPRAVTDLEWVRSNDKRLTQNYEAYSHLLCYLRGLNRQAATAELR 120
Db 71 EPDFNPRLGAETLPRAVTDLEWVRSNDKRLTQNYEAYSHLLCYLRGLNRQAATAELR 130
Oy 121 RSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 180
Db 131 RSLAHFCTSLQGLLSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDDFWLLKE 190
Oy 181 LQTLWRSKADFNRLKKMQPPAAAVTLHLGAHGF 215
Db 191 LQTLWRSKADFNRLKKMQPPAAAVTLHLGAHGF 225

RESULT 3
AAW56141
ID AAW56141 standard; Protein; 225 AA.
XX
AC AAW56141;

GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 13, 2003, 11:41:12 ; Search time 22.704 Seconds
(without alignments)
1261.843 Million cell updates/sec

Title: US-09-521-335-2

Perfect score: 1169

Sequence: 1 MLACLTVLWHLPAVPALNR.....KKMKQPPAAAVTLHLGAHF 215

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A Geneseq_101002.*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1169	100.0	215	AA19586	Human interleukin-
2	1169	100.0	225	AAW29715	Human neurotrophic
3	1169	100.0	225	AAW56141	Amino acid sequenc
4	1169	100.0	225	AAW94466	Human cardiostroph
5	1169	100.0	225	AAW87813	Human NNT-1 protei
6	1169	100.0	225	AAW63543	Amino acid sequenc
7	1169	100.0	225	AAW78176	Human novel neurot
8	1169	100.0	253	AAW25831	Human protein sequ
9	1169	100.0	321	ABB11896	Human cardiostroph
10	1169	100.0	321	AAW79399	Human protein SEQ

11	1162	99.4	260	22	AAW78415	Human protein SEQ
12	1157	99.0	223	22	AAE00828	Human cardiostroph
13	1136	97.2	215	21	AAE19587	Mouse interleukin-
14	1136	97.2	225	19	AAW29716	Mouse neurotrophic
15	1136	97.2	225	19	AAW56142	Amino acid sequenc
16	1136	97.2	225	21	AAW87814	Murine NNT-1 prote
17	1136	97.2	225	23	AAU78177	Mouse novel neurot
18	885	75.7	164	22	ABB40317	Peptide #7823 enco
19	885	75.7	164	22	ABB24716	Protein #6715 enco
20	885	75.7	164	22	AAW61118	Human brain expres
21	885	75.7	164	22	AAW73827	Human bone marrow
22	885	75.7	164	22	AAW20115	Peptide #5549 enco
23	885	75.7	164	22	AAW34012	Peptide #8049 enco
24	885	75.7	164	23	ABG43716	Human peptide enco
25	162.5	13.9	208	20	AAW09197	Human DNAX interle
26	160	13.7	208	16	AAW09196	Human DNAX interle
27	118.5	10.1	203	16	AAW83965	Mouse cardiac hype
28	118.5	10.1	203	17	AAW88204	Human cardiostroph
29	118.5	10.1	203	18	AAW29237	Murine cardiostroph
30	92	7.9	332	21	AAW22132	Arabidopsis thalia
31	92	7.9	332	21	AAW40321	Arabidopsis thalia
32	91.5	7.8	201	16	AAW83967	Human cardiac hype
33	91.5	7.8	201	18	AAW29238	Human cardiostroph
34	91.5	7.8	201	20	AAW06490	Human tumour-associ
35	91.5	7.8	201	21	AAW27662	Human protein PRO8
36	91.5	7.8	201	21	AAW13004	Human cardiostroph
37	91.5	7.8	201	21	AAW93697	Amino acid sequenc
38	91.5	7.8	201	21	AAW87818	Human cardiostroph
39	91.5	7.8	201	22	AAW50994	Human PRO882 prote
40	91	7.8	195	14	AAW34432	Sequence of growth
41	91	7.8	195	20	AAW83337	Chicken ciliary ne
42	91	7.8	1182	23	AAE19798	Mouse Hairless pro
43	90	7.7	232	22	AAU09152	Human cytokine Zal
44	90	7.7	232	23	AAU76374	Human helical prot
45	90	7.7	242	22	AAW20275	Human interleukin

ALIGNMENTS

RESULT 1
AA19586
ID AA19586 standard; Protein; 215 AA.
XX
AC AA19586;
XX 22-JAN-2001 (first entry)
XX Human interleukin-B60 (IL-B60).
DE Interleukin-B60; IL-B60; human; cytokine; cytokine-like factor-1;
KW haematopoietic; inflammation; antinflammatory; autoimmune disease;
KW therapy.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Peptide 1..17
FT Protein /label= Signal_peptide 18..215
FT /label= Mature-protein
XX
PN WO200053631-A1.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US06182.
XX
PR 11-MAR-1999; 99US-0267901.
XX
PA (SCHE) SCHERING CORP.
PI Oppmann B, Timans JC, Kastelein RA, Bazan JF;

RT and colon cancer derived by splicing to exon 11.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF492470; AAM18048.1; -;
KW Receptor.
SQ SEQUENCE 268 AA; 30705 MW; FBB498AB649A078C CRC64;

Query Match 14.9%; Score 333; DB 4; Length 268;
Best Local Similarity 36.6%; Pred. No. 3.2e-21;
Matches 83; Conservative 29; Mismatches 97; Indels 18; Gaps 8;

Qy 123 ILAGSLVVG-LPPEKPVNISCSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQD 181
Db 15 LFLNLCCLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTVHREGETLM 72
Qy 182 NTCEYHTVGHSPCHIPKD-LALFTPYEIWEATNRLGARSVDLTLDILDVTTDPPPD 240
Db 73 HECPDYITGGPNSCHFGKQYTSMTWRTYIMVNATNQMGSSFSDELYVDVTYIVQDPDPLE 132
Qy 241 VHSVGVGLEQLSQRVWV--SPPALKDF---LFQAKYQIRYRVSDVSKVVDVSNOTS 295
Db 133 LAV-EVKQPEDRKPYLWKWSPTLIDLTGWTFTLLYIRLKPKEAAEWE-IHFAGQOTE 190
Qy 296 CRLAGLKPGTVYFVQVRCNPGIYSGKAGIWSHPTAASTP 339
Db 191 FKILSLHPGQKYLVOVRCKP-----DHGYWSAWSPATFIQIPSGD 230

RESULT 7
Q96P36 PRELIMINARY; PRT; 288 AA.
AC Q96P36;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Prolactin receptor short isoform A.
GN PRUK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Trott J.F., Hovey R.C., Vonderhaar B.K.;
RT "Expression of two novel hPRLR isoforms in breast tumors.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF416618; AAL23914.1; -;
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN III.
DR Pfam; PF00041; fn3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 288 AA; 32760 MW; B45203EC045EB417 CRC64;

Query Match 14.9%; Score 332; DB 4; Length 288;
Best Local Similarity 37.1%; Pred. No. 4.3e-21;
Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;

Qy 123 ILAGSLVVG-LPPEKPVNISCSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQD 181
Db 15 LFLNLCCLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTVHREGETLM 72
Qy 182 NTCEYHTVGHSPCHIPKD-LALFTPYEIWEATNRLGARSVDLTLDILDVTTDPPPD 240
Db 73 HECPDYITGGPNSCHFGKQYTSMTWRTYIMVNATNQMGSSFSDELYVDVTYIVQDPDPLE 132
Qy 241 VHSVGVGLEQLSQRVWV--SPPALKDF---LFQAKYQIRYRVSDVSKVVDVSNOTS 295
Db 133 LAV-EVKQPEDRKPYLWKWSPTLIDLTGWTFTLLYIRLKPKEAAEWE-IHFAGQOTE 190
Qy 296 CRLAGLKPGTVYFVQVRCNPGIYSGKAGIWSHPTAASTP 339

Db 191 FKILSLHPGQKYLVOVRCKP-----DHGYWSAWSPATFIQIP 227
RESULT 8
Q9UHJ5 PRELIMINARY; PRT; 349 AA.
AC Q9UHJ5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Intermediate prolactin receptor isoform.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20054419; PubMed=10585417;
RA Kline J.B., Roehrs H., Clevenger C.V.;
RT "Functional characterization of the intermediate isoform of the human
RT prolactin receptor.";
RL J. Biol. Chem. 274:35461-35468(1999).
DR EMBL; AF166329; AAD49855.1; -;
DR HSP; P16471; IBP3.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM0060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 349 AA; 39806 MW; 932F20BE850CDD27 CRC64;

Query Match 14.9%; Score 332; DB 4; Length 349;
Best Local Similarity 37.1%; Pred. No. 5.6e-21;
Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;

Qy 123 ILAGSLVVG-LPPEKPVNISCSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYQD 181
Db 15 LFLNLCCLNGQLPPGKPEIFKCRSPNKETFTCWWRPGTDGG--LPTNYSLTVHREGETLM 72
Qy 182 NTCEYHTVGHSPCHIPKD-LALFTPYEIWEATNRLGARSVDLTLDILDVTTDPPPD 240
Db 73 HECPDYITGGPNSCHFGKQYTSMTWRTYIMVNATNQMGSSFSDELYVDVTYIVQDPDPLE 132
Qy 241 VHSVGVGLEQLSQRVWV--SPPALKDF---LFQAKYQIRYRVSDVSKVVDVSNOTS 295
Db 133 LAV-EVKQPEDRKPYLWKWSPTLIDLTGWTFTLLYIRLKPKEAAEWE-IHFAGQOTE 190
Qy 296 CRLAGLKPGTVYFVQVRCNPGIYSGKAGIWSHPTAASTP 339
Db 191 FKILSLHPGQKYLVOVRCKP-----DHGYWSAWSPATFIQIP 227

RESULT 9
Q96P35 PRELIMINARY; PRT; 376 AA.
AC Q96P35;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Prolactin receptor short isoform B.
GN PRLR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Trott J.F., Hovey R.C., Vonderhaar B.K.;
RT "Expression of two novel hPRLR isoforms in breast tumors.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

RT "Expression of multiple human prolactin receptor variants in breast

```
Best Local Similarity 99.0%; Pred. No. 1.2e-185;
Matches 406; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

Qy 1 MPAGRRGPAAGSARPPPLPPLLLLCVLGAPRAGSGAHTAVISPODPTLLIGSLLATC 60
Db 1 MPAGRRGPAAGSARPPPLPPLLLLCVLGAPRAGSGAHTAVISPODPTLLIGSLLATC 60
Qy 61 SVHGPPGATAGLWTLNGLRRLPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
Db 61 SVHGPPGATAGLWTLNGLRRLPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
Qy 121 GSILAGSCLYVGLPEKPNVSCWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGO 180
Db 121 GSILAGSCLYVGLPEKPNVSCWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGO 180
Qy 181 DNTCEEYHTVGPCHIPKDLALFTPYEIWEATNRLGSARSDVLTLDLDVVTTPDP 240
Db 181 DNTCEEYHTVGPCHIPKDLALFTPYEIWEATNRLGSARSDVLTLDLDVVTTPDP 240
Qy 241 VHSRVGGLDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLAG 300
Db 241 VHSRVGGLDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLAG 300
Qy 301 LKPGTVYFVQVRCNPFGLYGSKKAGIWEWSHPTAASTPRSERPGGACPRGGEPS 360
Db 301 LKPGTVYFVQVRCNPFGLYGSKKAGIWEWSHPTAASTPRSERPGGACPRGGEPS 360
Qy 361 GPVRELKQFLGWLKXKAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLP 407
Db 361 GPVRELKQFLGWLKXKAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILP 410

RESULT 2
Q9UH5 PRELIMINARY; PRT; 422 AA.
ID Q9UH5
AC Q9UH5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Class I cytokine receptor.
GN ZCYTOR5
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lok S., Presnell S.R., Jelmsberg A.C., Gilbert T., Whitmore T.E.,
Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.;
Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178684; AAD54385.1; -.
DR HSSP; P16471; 1BP3.
DR InterPro; IPR002396; CRIA.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR Receptor.
SQ SEQUENCE 422 AA; 46315 MW; 0D2C5F7A01B942EE CRC64;

Query Match 98.6%; Score 2198.5; DB 4; Length 422;
Best Local Similarity 98.8%; Pred. No. 2.7e-185;
Matches 405; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

Qy 1 MPAGRRGPAAGSARPPPLPPLLLLCVLGAPRAGSGAHTAVISPODPTLLIGSLLATC 60
Db 1 MPAGRRGPAAGSARPPPLPPLLLLCVLGAPRAGSGAHTAVISPODPTLLIGSLLATC 60
Qy 61 SVHGPPGATAGLWTLNGLRRLPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
Db 61 SVHGPPGATAGLWTLNGLRRLPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
Qy 121 GSILAGSCLYVGLPEKPNVSCWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGO 180
Db 121 GSILAGSCLYVGLPEKPNVSCWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGO 180
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Db 121 GSILAGSCLYVGLPEKPNVSCWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGO 180
Qy 181 DNTCEEYHTVGPCHIPKDLALFTPYEIWEATNRLGSARSDVLTLDLDVVTTPDP 240
Db 181 DNTCEEYHTVGPCHIPKDLALFTPYEIWEATNRLGSARSDVLTLDLDVVTTPDP 240
Qy 241 VHSRVGGLDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLAG 300
Db 241 VHSRVGGLDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTSCLAG 300
Qy 301 LKPGTVYFVQVRCNPFGLYGSKKAGIWEWSHPTAASTPRSERPGGACPRGGEPS 360
Db 301 LKPGTVYFVQVRCNPFGLYGSKKAGIWEWSHPTAASTPRSERPGGACPRGGEPS 360
Qy 361 GPVRELKQFLGWLKXKAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLP 407
Db 361 GPVRELKQFLGWLKXKAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILP 410

RESULT 3
Q9JM58 PRELIMINARY; PRT; 425 AA.
ID Q9JM58
AC Q9JM58;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytokine receptor like molecule 3 precursor.
GN CRLF1 OR CRLF3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Hiroshima T., Iwama A., Nakamura Y., Nakauchi H.;
Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040038; BAA92777.1; -.
DR HSSP; P16471; 1BP3.
DR MGD; MGI:1340030; Crlf1.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
DR Receptor; Signal.
FT SIGNAL 1 34 POTENTIAL.
SQ SEQUENCE 425 AA; 46662 MW; 910535C629CA7056 CRC64;

Query Match 93.9%; Score 2095; DB 11; Length 425;
Best Local Similarity 93.9%; Pred. No. 3.5e-176;
Matches 388; Conservative 6; Mismatches 13; Indels 6; Gaps 3;

Qy 1 MPAGRRGPAAGSARPP-PLLP-LL-LLLCVLGAPRAGSGAHTAVISPODPTLLIGSLL 57
Db 1 MPAGRRGPAAGSARPPPLPPLSLLSLLSLLSLLSLLSLLSLLSLLSLLSLL 60
Qy 58 ATCSVHGPPGATAGLWTLNGLRRLPELSRVLNASTLALANLNGSRQSGDNLVCH 117
Db 61 ATCSVHGPPGATAGLWTLNGLRRLPELSRVLNASTLALANLNGSRQSGDNLVCH 120
Qy 118 ARDSILAGSCLYVGLPEKPNVSCWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 177
Db 121 ARDSILAGSCLYVGLPEKPNVSCWKNMKDLTCRWTPGAHGETFLHTNYSKYKLRW 180
Qy 178 YGQDNTCEEYHTVGPCHIPKDLALFTPYEIWEATNRLGSARSDVLTLDLDVVTTP 237
Db 181 YGQDNTCEEYHTVGPCHIPKDLALFTPYEIWEATNRLGSARSDVLTLDLDVVTTP 240
Qy 238 PPDVHVSRVGGLDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTS 297
Db 241 PPDVHVSRVGGLDQLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVDDVSNQTS 300
Qy 298 LAGLPGTVYFVQVRCNPFGLYGSKKAGIWEWSHPTAASTPRSERPGGACPRGGE 357
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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 11:46:42 ; Search time 35.424 Seconds
(without alignments)
2384.805 Million cell updates/sec

Title: US-09-521-335-12
Perfect score: 2230
Sequence: 1 MPAGRRGPAQAARRPPPL.....WRAWMQSHKTRNQVLPDKL 410

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues
Number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvrius.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2202.5	98.8	422	4	075462
2	2198.5	98.6	422	4	Q9UHH5
3	2095	93.9	425	11	Q9JMS8
4	365.5	16.4	918	13	Q9W6U9
5	354	15.9	881	13	Q57519
6	333	14.9	268	4	Q8TD78
7	332	14.9	288	4	Q96P36
8	332	14.9	349	4	Q9UHH5
9	332	14.9	376	4	Q96P35
10	325.5	14.6	206	4	Q16354
11	317	14.2	622	6	Q9N0J7
12	309.5	13.9	608	11	Q99JZ1
13	294	13.2	611	13	Q9PTH9
14	292.5	13.1	611	13	Q9IBF6
15	292.5	13.1	611	13	Q9PTI0
16	290	13.0	626	13	Q90WG7

17	270.5	12.1	227	6	Q9GLW3
18	270.5	12.1	346	13	Q93404
19	270.5	12.1	625	6	Q9XS92
20	270	12.1	636	13	Q90Z16
21	261.5	11.7	538	13	Q9DFU0
22	261	11.7	638	13	Q9DE08
23	246	11.0	861	6	Q9BEG2
24	243.5	10.9	197	4	Q8TD76
25	243.5	10.9	1147	13	Q9DDK1
26	242.5	10.9	217	4	Q8TD75
27	242.5	10.9	1148	13	Q9IBA7
28	240	10.8	600	13	Q9PTP0
29	238.5	10.7	848	6	Q8WN24
30	237	10.6	372	11	Q88507
31	237	10.6	1146	13	Q918V6
32	236	10.6	604	13	Q8QG54
33	235.5	10.6	217	6	Q46386
34	233.5	10.5	509	4	Q8WYJ0
35	231.5	10.4	198	6	Q18985
36	211.5	9.5	422	4	Q16542
37	208.5	9.3	432	11	Q64385
38	208	9.3	431	11	Q99MF4
39	200.5	9.0	1083	13	Q8QFQ7
40	199.5	8.9	432	11	P70225
41	195.5	8.8	1162	11	Q9QWG3
42	193.5	8.7	848	6	Q9MZS2
43	193.5	8.7	1165	6	O02671
44	192.5	8.6	710	13	O57520
45	184	8.3	895	11	Q62960

ALIGNMENTS

RESULT 1

075462	PRELIMINARY;	PRT;	422 AA.
AC	075462;		
DT	01-NOV-1998 (TrEMBLrel. 08, Created)		
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)		
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)		
DE	Cytokine-like factor-1 precursor.		
GN	CLF-1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Elson G.C.A., Graber P., Losberger P., Herren S., Gretener D.,		
RA	Menoud L.N., Wells T.N.C., Kosco-Vilbois M.H., Gauchat J.F.;		
RT	"CLF-1, a Novel Soluble Protein Shares Homology With Members of the		
RT	Cytokine Type-I Receptor Family."		
RL	J. Immunol. 0:0-0(1998).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Magrangeas F., Jacques Y., Minvielle S.;		
RT	"Cloning and expression of a novel soluble protein containing		
RT	hematopoietic cytokine receptor domains."		
RL	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF059293; AAC28335.1; -		
DR	EMBL; AF073515; AAD39681.1; -		
DR	HSSP; P16471; 1BP3		
DR	InterPro; IPR002996; CRIA.		
DR	InterPro; IPR003961; FN_III.		
DR	Pfam; PF00041; fn3; 2.		
DR	SMART; SM00060; FN3; 2.		
KW	Receptor; Signal.		
FT	SIGNAL 1 37 POTENTIAL		
FT	CHAIN 38 422 CYTOKINE-LIKE FACTOR-1.		
SQ	SEQUENCE 422 AA; 46301 MW; AD9DFCB01B84228 CRC64;		

Query Match 98.8%; Score 2202.5; DB 4; Length 422;

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 11:41:52 ; Search time 11.808 Seconds
(without alignments)
1440.150 Million cell updates/sec

Title: US-09-521-335-12

Perfect score: 2230

Sequence: 1 MPAGRRGPAQAARPPPL.....WRAMQKSHKTRNQVLDPKL 410

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Se: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	332	14.9	622	1	PRLR_HUMAN
2	323	14.5	918	1	IL6B_HUMAN
3	317.5	14.2	917	1	IL6B_MOUSE
4	316	14.2	830	1	PRLR_COLLI
5	314.5	14.1	918	1	IL6B_RAT
6	313	14.0	610	1	PRLR_RAT
7	309.5	13.9	581	1	PRLR_SHEEP
8	309.5	13.9	608	1	PRLR_MOUSE
9	308	13.8	831	1	PRLR_CHICK
10	307	13.8	831	1	PRLR_MELGA
11	306.5	13.7	581	1	PRLR_BOVIN
12	304	13.6	581	1	PRLR_CEREL
13	300.5	13.5	616	1	PRLR_RABIT
14	263.5	11.8	630	1	PRLR_ORENI
15	256	11.5	837	1	GCSR_MOUSE
16	246	11.0	372	1	CNTR_RAT
17	243	10.9	836	1	GCSR_HUMAN
18	233.5	10.5	372	1	CNTR_HUMAN
19	223	10.0	467	1	IL6A_PIG
20	213	9.6	862	1	IL2S_HUMAN
21	211.5	9.5	362	1	CNTR_CHICK
22	205.5	9.2	874	1	IL2S_MOUSE
23	201.5	9.0	460	1	IL6A_MOUSE
24	201	9.0	468	1	IL6A_HUMAN
25	200	9.0	1097	1	LIFR_HUMAN
26	198.5	8.9	462	1	IL6A_RAT
27	194.5	8.7	1162	1	LEPR_MOUSE
28	194	8.7	625	1	TPOR_MOUSE
29	190.5	8.5	1162	1	LEPR_RAT
30	187	8.4	1092	1	LIFR_MOUSE
31	186.5	8.4	635	1	TPOR_HUMAN
32	178	8.0	1165	1	LEPR_HUMAN
33	169.5	7.6	427	1	IL31_HUMAN

34	165.5	7.4	638	1	GHR_RABIT
35	161.5	7.2	508	1	EPOR_HUMAN
36	160	7.2	888	1	UFO_MOUSE
37	158.5	7.1	638	1	GHR_PIG
38	158	7.1	507	1	EPOR_RAT
39	156	7.0	507	1	EPOR_MOUSE
40	153	6.9	638	1	GHR_HUMAN
41	152	6.8	424	1	IL31_MOUSE
42	151	6.8	1040	1	AXOI_RAT
43	151	6.8	2012	1	DSCA_HUMAN
44	150.5	6.7	897	1	CYRB_HUMAN
45	148.5	6.7	1036	1	AXOI_CHICK

ALIGNMENTS

RESULT 1
PRLR_HUMAN
ID PRLR_HUMAN STANDARD; PRT; 622 AA.
AC P16471; Q9BX87;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN PRLR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=90114212; PubMed=2558309;
RA Boutin J.-M., Edery M., Shiota M., Jolicoeur C., Lesueur L.,
RA Ali S., Gould D., Djiane J., Kelly P.A.;
RT "Identification of a cDNA encoding a long form of prolactin receptor
RT in human hepatoma and breast cancer cells.";
RL Mol. Endocrinol. 3:1455-1461(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=99182102; PubMed=10084611;
RA Hu Z.-Z., Zhuang L., Meng J., Leonides M., Dufau M.L.;
RT "The human prolactin receptor gene structure and alternative promoter
RT utilization: the generic promoter hPII and a novel human promoter
RT hP(N)".
RL J. Clin. Endocrinol. Metab. 84:1153-1156(1999).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX TISSUE=Breast carcinoma;
RA Kline J.B., Clevenger C.V.;
RT "Characterization of a novel and functional human prolactin receptor
RT isoform (Delta-S1 PRLr) containing only one extracellular
RT fibronectin-like domain.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 25-235.
RX MEDLINE=95075462; PubMed=7984244;
RA Somers W., Ultsch M., de Vos A.M., Kossiakoff A.A.;
RT "The X-ray structure of a growth hormone-prolactin receptor complex.";
RL Nature 372:478-481(1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
PROLACTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/Delta-S1;
CC are produced by alternative splicing.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright.. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial

Qy 296 CRLAGLKPGTVYFVQVRCNPGIYKSKAGIWSHPTAASTP 339
Db 191 FKILSLHPGQKYLQVRCCKP-----DHGYWSAWSPATFIQIP 227

RESULT 2
A:Accession: A59405
A:Molecule type: mRNA
A:Residues: 1-622 <BOU>
A:Cross-references: GB:M31661; NID:g190361; PIDN:AAA60174.1; PID:g190362
R:Fuh, G.; Wells, J.A.
J. Biol. Chem. 270, 13133-13137, 1995
A:Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell li.
A:Reference number: A57018
A:Accession: A57018
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 25-228, 'AW' <RES>
A:Cross-references: GB:S78505; NID:g999114; PIDN:AAB34470.1; PID:g999115
C:Genetics:
A:Gene: GDB:PRLR
A:Cross-references: GDB:120315; OMIM:176761
A:Map position: 5p13.3-5p13.1
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-622/Product: prolactin receptor, long form #status predicted <MAT>
F:36-221/Domain: cytokine receptor homology <CRS>
F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.9%; Score 332; DB 2; Length 622;
Best Local Similarity 37.1%; Pred. No. 3.9e-18;
Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;

Qy 123 ILAGSCLVYG-LPPEKPNVISCWKNMKDLTCRWTPGAHGETFLHTNYSLKVKLRWYQGD 181
Db 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTTCWRRPGTDGG--LPTNYSLTYYHREGETLM 72

Qy 182 NTCBEYHTVGPHSCHPKD-LALFTPYEIVWEATNRLGARSDDLTLTDLVDVTTDPPPD 240
Db 73 HECPDYITGGNSCHFGKQYTMRTYIMVNTATNQMGSSFSDELYVDVTVYVQDPDPLE 132

Qy 241 VHVSRVGGLEDQLSVRWV--SPALKDF---LFOAKYQIRYRVESVDWKVDDVSNQTS 295
Db 133 LAV-EVKQPEDKRPYLWIKWSPPTLIDLTGTFWTLTYEIRLKPKEAEWE-IHFAGQOTE 190

Qy 296 CRLAGLKPGTVYFVQVRCNPGIYKSKAGIWSHPTAASTP 339
Db 191 FKILSLHPGQKYLQVRCCKP-----DHGYWSAWSPATFIQIP 227

RESULT 4
A36337
membrane glycoprotein gpl30 precursor - human
C:Species: Homo sapiens (man)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 28-Jul-2000
C:Accession: A36337
R:Hibi, M.; Murakami, M.; Saito, M.; Hirano, T.; Taga, T.; Kishimoto, T.
Cell 63, 1149-1157, 1990
A:Title: Molecular cloning and expression of an IL-6 signal transducer, gpl30.
A:Reference number: A36337; MUID:9108484; PMID:2261637
A:Accession: A36337
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-918 <HIB>
A:Cross-references: GB:M57230; NID:g186353; PIDN:AAA59155.1; PID:g186354
C:Genetics:
A:Gene: GDB:IL6ST; GPl30
A:Cross-references: GDB:126725; OMIM:600694
A:Map position: 5q11-5q11
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; membrane protein
F:134-316/Domain: cytokine receptor homology <CRS>

Query Match 14.5%; Score 323; DB 2; Length 918;
Best Local Similarity 28.2%; Pred. No. 3.2e-17;
Matches 87; Conservative 52; Mismatches 151; Indels 18; Gaps 8;

Qy 43 ISPODPTLLIGSSLATCSVHG---DPPGATAEGLYWTNGRRLLPPELSRVLNASTLALA 99

Qy 296 CRLAGLKPGTVYFVQVRCNPGIYKSKAGIWSHPTAASTP 339
Db 191 FKILSLHPGQKYLQVRCCKP-----DHGYWSAWSPATFIQIP 227

RESULT 2
A:Accession: A59405
A:Molecule type: mRNA
A:Residues: 1-622 <BOU>
A:Cross-references: GB:M31661; NID:g190361; PIDN:AAA60174.1; PID:g190362
R:Fuh, G.; Wells, J.A.
J. Biol. Chem. 270, 13133-13137, 1995
A:Title: Prolactin receptor antagonists that inhibit the growth of breast cancer cell li.
A:Reference number: A57018
A:Accession: A57018
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 25-228, 'AW' <RES>
A:Cross-references: GB:S78505; NID:g999114; PIDN:AAB34470.1; PID:g999115
C:Genetics:
A:Gene: GDB:PRLR
A:Cross-references: GDB:120315; OMIM:176761
A:Map position: 5p13.3-5p13.1
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-622/Product: prolactin receptor, short form #status predicted <MAT>
F:36-221/Domain: cytokine receptor homology <CRS>
F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.9%; Score 332; DB 2; Length 376;
Best Local Similarity 37.1%; Pred. No. 2.1e-18;
Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;

Qy 123 ILAGSCLVYG-LPPEKPNVISCWKNMKDLTCRWTPGAHGETFLHTNYSLKVKLRWYQGD 181
Db 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFTTCWRRPGTDGG--LPTNYSLTYYHREGETLM 72

Qy 182 NTCBEYHTVGPHSCHPKD-LALFTPYEIVWEATNRLGARSDDLTLTDLVDVTTDPPPD 240
Db 73 HECPDYITGGNSCHFGKQYTMRTYIMVNTATNQMGSSFSDELYVDVTVYVQDPDPLE 132

Qy 241 VHVSRVGGLEDQLSVRWV--SPALKDF---LFOAKYQIRYRVESVDWKVDDVSNQTS 295
Db 133 LAV-EVKQPEDKRPYLWIKWSPPTLIDLTGTFWTLTYEIRLKPKEAEWE-IHFAGQOTE 190

Qy 296 CRLAGLKPGTVYFVQVRCNPGIYKSKAGIWSHPTAASTP 339
Db 191 FKILSLHPGQKYLQVRCCKP-----DHGYWSAWSPATFIQIP 227

RESULT 3
A40144
prolactin receptor long form precursor, hepatoma and breast cancer cells - human
C:Species: Homo sapiens (man)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 01-Dec-2000
C:Accession: A40144; A57018
R:Boutin, J.M.; Edery, M.; Shiota, M.; Jolicoeur, C.; Lesueur, L.; Ali, S.; Gould, D.; Mol. Endocrinol. 3, 1455-1461, 1989
A:Title: Identification of a cDNA encoding a long form of prolactin receptor in human he
A:Reference number: A40144; MUID:90114212; PMID:2558309

GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 11:48:13 ; Search time 18.368 Seconds
(without alignments)
2145.858 Million cell updates/sec

Title: US-09-521-335-12

Perfect score: 2230

Sequence: 1 MPAGRRGPAQAQARRPPPLL.....WRAMQKSHKTRNQLPDKL 410

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	332	14.9	288	2 B59405	prolactin receptor
2	332	14.9	376	2 A59405	prolactin receptor
3	332	14.9	622	2 A40144	prolactin receptor
4	323	14.5	918	2 A36337	membrane glycoprot
5	317.5	14.2	917	2 I49699	glycoprotein 130 -
6	316	14.2	830	2 I50455	prolactin receptor
7	314.5	14.1	918	2 A44257	interleukin-6 sign
8	313	14.0	310	2 A29884	prolactin receptor
9	313	14.0	412	2 A41070	prolactin receptor
10	313	14.0	610	2 A34631	lactogen receptor
11	313	14.0	610	2 A36116	prolactin receptor
12	309.5	13.9	292	2 I77525	prolactin receptor
13	309.5	13.9	303	2 I77524	prolactin receptor
14	309.5	13.9	608	2 I53269	prolactin receptor
15	308	13.8	831	2 JQ1655	prolactin receptor
16	306.5	13.7	581	2 I45971	prolactin receptor
17	300.5	13.5	616	2 A30304	prolactin receptor
18	263.5	11.8	630	2 I51086	prolactin receptor
19	256	11.5	837	2 A34898	granulocyte colony
20	246	11.0	372	2 I58441	ciliary neurotroph
21	243	10.9	771	2 B38252	granulocyte colony
22	243	10.9	783	2 JH0329	granulocyte colony
23	243	10.9	863	2 J38252	granulocyte colony
24	235.5	10.6	372	1 UHUUCN	ciliary neurotroph
25	211.5	9.5	362	2 S60614	growth promoting a
26	211.5	9.5	422	2 I37891	interleukin-11 rec
27	208.5	9.3	432	2 I48343	interleukin-11 rec
28	201.5	9.0	460	2 JL0145	interleukin-6 rece
29	201	9.0	468	1 A41242	interleukin-6 rece

RESULT 1

B59405

prolactin receptor short form Sib precursor, breast cancer cells T-47D - human
C:Species: Homo sapiens (man)

C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Mar-2002

C/Accession: B59405; B49400

R/Hu. Z.Z.; Meng, J.; Dufau, M.L.

J. Biol. Chem. 276, 41086-41094, 2001

A>Title: Isolation and characterization of two novel forms of the human prolactin receptor

A/Reference number: A59405; MUID:21538812; PMID:11518703

A/Accession: B59405

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-288 <HU>

A/Cross-references: GB:AF214012; PIDN:AF214012.1

R/Hu. Z.Z.

submitted to GenBank, December, 1999

A/Reference number: A49400

A/Accession: B49400

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-288 <HU>

A/Cross-references: GB:AF214012; PIDN:AF214012.1

C/Comment: This is one of the short forms (Sla and Sib) of the human proactin receptor gene
ta-casein gene promoter activation, with Sib more effective than Sla. However, their ligand

C/Genetics:

A/Gene: GDB:PRLR

A/Cross-references: GDB:120315; OMIM:176761

A/Map position: 5p13.3-5p13.1

C/Superfamily: cytokine receptor homology

C/Keywords: glycoprotein; transmembrane protein

F;1-24/Domain: signal sequence #status predicted <SIG>

F;25-288/Product: prolactin receptor, short form Sib #status predicted <MAT>

F;36-221/Domain: cytokine receptor homology <CRS>

F;59,104,233/Binding site: carbohydrate (Asn) #status predicted

Query Match

14.9%; Score 332; DB 2; Length 288;

Best Local Similarity 37.1%; Pred. No. 1.5e-18;

Matches 83; Conservative 28; Mismatches 95; Indels 18; Gaps 8;

QY 123 ILAGSCLYVG-LPPEKPVNISCKNNKDLTCRWTPGAHGETFLHTNYSLSKYKLRWYQD 181

Db 15 LFLNTCLLNGQLPPGKPEIFKCRSPNKETFCWVRGTDGG--LPTNYSLSLYHREGETLM 72

QY 182 NTCEYHTVGPCHSHPKO-LALFTPYEIVWEATNRLGARSVDLTLDLDVTTTDPDPPD 240

Db 73 HECFDYITGPNSCFHGKQYTSWRTYIMVNATNQMGSSFSDELYVDVTYIVQPPPLE 132

QY 241 VHSRVRGGLDQLSRWV--SPALKDF---LFOAKYQIYRYVEDSDVKVVDVDSNQS 295

Db 133 LAV-EVKQPEDRKPRYLWIKWSPPTLIDLKTGWFTLLYELRLKPEKAEWB-IHFAGQOTE 190

; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-944-862-32

Query Match 98.8%; Score 2202.5; DB 10; Length 422;
Best Local Similarity 99.08; Pred No. 3.8e-157;
Matches 406; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

Qy 1 MPAGRRGPAQASARRPPPLPLLLLLVCVLPAGPRAGSGAHTAVISPDPTLLIGSSLATC 60
1 MPAGRRGPAQASARRPPPLPLLLLLVCVLPAGPRAGSGAHTAVISPDPTLLIGSSLATC 60
Qy 61 SVHGDPGATAGLWTLNGLRRLPELSRVLNASTLALANLNGSRORSQDNLVCHARD 120
61 SVHGDPGATAGLWTLNGLRRLPELSRVLNASTLALANLNGSRORSQDNLVCHARD 120
Db 61 SVHGDPGATAGLWTLNGLRRLPELSRVLNASTLALANLNGSRORSQDNLVCHARD 120
Qy 121 GSILAGSLVGLPPEKPVNTSCWSKNMKDLTCRWTPCAHGETFLHTNYSKYLKRWYQ 180
121 GSILAGSLVGLPPEKPVNTSCWSKNMKDLTCRWTPCAHGETFLHTNYSKYLKRWYQ 180
Db 121 GSILAGSLVGLPPEKPVNTSCWSKNMKDLTCRWTPCAHGETFLHTNYSKYLKRWYQ 180
Qy 181 DNTCEEYHTVGHPSCHIPKDLALFTPYEIVWEATNRLGARSQDVLTLIDLVVTTDPPD 240
181 DNTCEEYHTVGHPSCHIPKDLALFTPYEIVWEATNRLGARSQDVLTLIDLVVTTDPPD 240
Db 181 DNTCEEYHTVGHPSCHIPKDLALFTPYEIVWEATNRLGARSQDVLTLIDLVVTTDPPD 240
Qy 241 VHSVVGLEQLSVRVVSPALPKDFLQAKYQIRYVEDSDVWKVDDVNSQTSCLAG 300
241 VHSVVGLEQLSVRVVSPALPKDFLQAKYQIRYVEDSDVWKVDDVNSQTSCLAG 300
Db 241 VHSVVGLEQLSVRVVSPALPKDFLQAKYQIRYVEDSDVWKVDDVNSQTSCLAG 300
Qy 301 LKPGTVYFVQVRCNPFGLYGGKAGIWEWSHPTAASTPRSRPFGGACPRGGEPS 360
301 LKPGTVYFVQVRCNPFGLYGGKAGIWEWSHPTAASTPRSRPFGGACPRGGEPS 360
Db 301 LKPGTVYFVQVRCNPFGLYGGKAGIWEWSHPTAASTPRSRPFGGACPRGGEPS 360
Qy 361 GPVRELKQFLGWLKXKHYACNSLFRYLDQWRAMQKSHKTRNQ---VLP 407
361 GPVRELKQFLGWLKXKHYACNSLFRYLDQWRAMQKSHKTRNQDEGILP 410
Db 361 GPVRELKQFLGWLKXKHYACNSLFRYLDQWRAMQKSHKTRNQDEGILP 410

RESULT 12
9-945-587-32
Sequence 32, Application US/09945587
Patent No. US20020127643A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Klavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tomas, Daniel
; APPLICANT: Wood, William
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/945,587
; CURRENT FILING DATE: 2001-09-26

; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108
; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020127643A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020127643A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678

;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 32
;; LENGTH: 422
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-944-457-32

Query Match 98.8%; Score 2202.5; DB 10; Length 422;
At Local Similarity 99.0%; Pred. No. 3.8e-157;
Matches 406; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

Qy 1 MPACRRGPAQASARRPPPLPPLLLCVLGPAPRAGSGAHTAVISPODPTLLIGSSILATC 60
Db 1 MPACRRGPAQASARRPPPLPPLLLCVLGPAPRAGSGAHTAVISPODPTLLIGSSILATC 60
Qy 61 SVHGDPGCAETAAGLYWTNGRRRLPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
Db 61 SVHGDPGCAETAAGLYWTNGRRRLPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
Qy 121 GSIIAGSLYVGLPPEKPVNISCNKNMKOLTCRWTPGAHGETFLHNTYSKYKLRWYG 180
Db 121 GSIIAGSLYVGLPPEKPVNISCNKNMKOLTCRWTPGAHGETFLHNTYSKYKLRWYG 180
Qy 181 DNTCEEVHTVGPSPHCHIPKDALSTPEIWEATNRIGSARSDVLTDLDDVTTDPPD 240
Db 181 DNTCEEVHTVGPSPHCHIPKDALSTPEIWEATNRIGSARSDVLTDLDDVTTDPPD 240
Qy 241 VHSRVGGLDQLSVRVVSPPALKDFLFOAKYQIRYRVSDVMKWVDDVSNQTSCLAG 300
Db 241 VHSRVGGLDQLSVRVVSPPALKDFLFOAKYQIRYRVSDVMKWVDDVSNQTSCLAG 300
Qy 301 LKPTVTVFQVRCNPFPGIYSGKKAGINSEWSHPTAATPSRERPGGGACPRGGPSS 360
Db 301 LKPTVTVFQVRCNPFPGIYSGKKAGINSEWSHPTAATPSRERPGGGACPRGGPSS 360
Qy 361 GPVRELKQFLGWLKKHAYCSNLSFRIDYQDRAWMQSKHTRNQ---VLP 407
Db 361 GPVRELKQFLGWLKKHAYCSNLSFRIDYQDRAWMQSKHTRNQDEGILP 410

RESULT 11
US-09-944-862-32
; Sequence 32, Application US/09944862
; Patent No. US20020115145A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tomas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

;; TITLE OF INVENTION: ACIDS ENCODING THE SAME
;; FILE REFERENCE: P2548P1C1
;; CURRENT APPLICATION NUMBER: US/09/944,862
;; CURRENT FILING DATE: 2001-09-26
;; PRIOR APPLICATION NUMBER: 09/866,028
;; PRIOR FILING DATE: 2001-05-25
;; PRIOR APPLICATION NUMBER: 60/067,411
;; PRIOR FILING DATE: December 3, 1997
;; PRIOR APPLICATION NUMBER: 60/069,334
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,335
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,278
;; PRIOR FILING DATE: December 11, 1997
;; PRIOR APPLICATION NUMBER: 60/069,425
;; PRIOR FILING DATE: December 12, 1997
;; PRIOR APPLICATION NUMBER: 60/069,696
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,694
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,702
;; PRIOR FILING DATE: December 16, 1997
;; PRIOR APPLICATION NUMBER: 60/069,870
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/069,873
;; PRIOR FILING DATE: December 17, 1997
;; PRIOR APPLICATION NUMBER: 60/068,017
;; PRIOR FILING DATE: December 18, 1997
;; PRIOR APPLICATION NUMBER: 60/070,440
;; PRIOR FILING DATE: January 5, 1998
;; PRIOR APPLICATION NUMBER: 60/074,086
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/074,092
;; PRIOR FILING DATE: February 9, 1998
;; PRIOR APPLICATION NUMBER: 60/075,945
;; PRIOR FILING DATE: February 25, 1998
;; PRIOR APPLICATION NUMBER: 60/112,850
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 60/113,296
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 60/146,222
;; PRIOR FILING DATE: July 28, 1999
;; PRIOR APPLICATION NUMBER: PCT/US98/19330
;; PRIOR FILING DATE: September 16, 1998
;; PRIOR APPLICATION NUMBER: PCT/US98/25108
;; PRIOR FILING DATE: December 1, 1998
;; PRIOR APPLICATION NUMBER: 09/216,021
;; PRIOR FILING DATE: December 16, 1998
;; PRIOR APPLICATION NUMBER: 09/218,517
;; PRIOR FILING DATE: December 22, 1998
;; PRIOR APPLICATION NUMBER: 09/254,311
;; PRIOR FILING DATE: March 3, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/12252
;; PRIOR FILING DATE: June 22, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/21090
;; PRIOR FILING DATE: September 15, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28409
;; PRIOR FILING DATE: No. US20020115145A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: No. US20020115145A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042

PRIOR FILING DATE: February 11, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: February 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/05841
 PRIOR FILING DATE: March 2, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/08439
 PRIOR FILING DATE: March 30, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/14042
 PRIOR FILING DATE: May 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/20710
 PRIOR FILING DATE: July 28, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/32678
 PRIOR FILING DATE: December 1, 2000
 PRIOR APPLICATION NUMBER: PCT/US01/06520
 PRIOR FILING DATE: February 28, 2001
 NUMBER OF SEQ ID NOS: 120
 SEQ ID NO 32
 LENGTH: 422
 TYPE: PRT
 ORGANISM: Homo Sapien
 9-944-449-32

Query Match 98.8%; Score 2202.5; DB 10; Length 422;
 Best Local Similarity 99.0%; Pred. No. 3.8e-157;
 Matches 406; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

Qy	1	MPAGRRGPAASARRPPPLLLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC	60
Db	1	MPAGRRGPAASARRPPPLLLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC	60
Qy	61	SVHGDPGATAGLYWTNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD	120
Db	61	SVHGDPGATAGLYWTNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD	120
Qy	121	GSILAGSLYGLPPEKPVNISCWSKMKDLTCRWTPGAHGETFLHTNYSKYKLRYGQ	180
Db	121	GSILAGSLYGLPPEKPVNISCWSKMKDLTCRWTPGAHGETFLHTNYSKYKLRYGQ	180
Qy	181	DNTCEEVHTGPHSCHIPKDLALFTPEIWEATNRLGARSDDVLTLDILVDVTTDPPD	240
Db	181	DNTCEEVHTGPHSCHIPKDLALFTPEIWEATNRLGARSDDVLTLDILVDVTTDPPD	240
Qy	241	VHVSRRVGSLEQLSVRWVSPALPKDFLQAKYQIRYRVSDVMKWVDDVSNQTSCLAG	300
Db	241	VHVSRRVGSLEQLSVRWVSPALPKDFLQAKYQIRYRVSDVMKWVDDVSNQTSCLAG	300
Qy	301	LKPGTVFVQVRCNPFPGIYGSKKAGIWSHPTAASTPRSERPGPGGACPRGGEPS	360
Db	301	LKPGTVFVQVRCNPFPGIYGSKKAGIWSHPTAASTPRSERPGPGGACPRGGEPS	360
Qy	361	GPVRELKQFLGWLKKGAYCSNLSFRLLYDQWRAMQKSHKTRNQ---	407
Db	361	GPVRELKQFLGWLKKGAYCSNLSFRLLYDQWRAMQKSHKTRNQDEGILP	410

RESULT 10
 US-09-944-457-32
 Sequence 32, Application US/09944457
 Patent No. US20020110859A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
 APPLICANT: Botstein, David
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Geritsen, Mary
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul
 APPLICANT: Grimaldi, Christopher
 APPLICANT: Gurney, Austin
 APPLICANT: Hillan, Kenneth
 APPLICANT: Kljavin, Ivar
 APPLICANT: Napier, Mary

APPLICANT: Roy, Margaret
 APPLICANT: Tumas, Daniel
 APPLICANT: Wood, William
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P2548P1C1
 CURRENT APPLICATION NUMBER: US/09/944,457
 CURRENT FILING DATE: 2001-09-26
 PRIOR APPLICATION NUMBER: 09/866,028
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/067,411
 PRIOR FILING DATE: December 3, 1997
 PRIOR APPLICATION NUMBER: 60/069,334
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,335
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,278
 PRIOR FILING DATE: December 11, 1997
 PRIOR APPLICATION NUMBER: 60/069,425
 PRIOR FILING DATE: December 12, 1997
 PRIOR APPLICATION NUMBER: 60/069,696
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,694
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,702
 PRIOR FILING DATE: December 16, 1997
 PRIOR APPLICATION NUMBER: 60/069,870
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/069,873
 PRIOR FILING DATE: December 17, 1997
 PRIOR APPLICATION NUMBER: 60/068,017
 PRIOR FILING DATE: December 18, 1997
 PRIOR APPLICATION NUMBER: 60/070,440
 PRIOR FILING DATE: January 5, 1998
 PRIOR APPLICATION NUMBER: 60/074,086
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/074,092
 PRIOR FILING DATE: February 9, 1998
 PRIOR APPLICATION NUMBER: 60/075,945
 PRIOR FILING DATE: February 25, 1998
 PRIOR APPLICATION NUMBER: 60/112,850
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 60/113,296
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 60/146,222
 PRIOR FILING DATE: July 28, 1999
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 PRIOR FILING DATE: December 1, 1998
 PRIOR APPLICATION NUMBER: 09/216,021
 PRIOR FILING DATE: December 16, 1998
 PRIOR APPLICATION NUMBER: 09/218,517
 PRIOR FILING DATE: December 22, 1998
 PRIOR APPLICATION NUMBER: 09/254,311
 PRIOR FILING DATE: March 3, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/12252
 PRIOR FILING DATE: June 22, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/21090
 PRIOR FILING DATE: September 15, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28409
 PRIOR FILING DATE: NO. US20020110859A1ember 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28313
 PRIOR FILING DATE: NO. US20020110859A1ember 30, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/28301
 PRIOR FILING DATE: December 1, 1999
 PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR FILING DATE: December 16, 1999
 PRIOR APPLICATION NUMBER: PCT/US00/03565
 PRIOR FILING DATE: February 11, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR FILING DATE: February 22, 2000
 PRIOR APPLICATION NUMBER: PCT/US00/05841

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; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; Q ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-866-028-32

Query Match          98.8%; Score 2202.5; DB 10; Length 422;
Best Local Similarity 99.0%; Pred. No. 3.8e-157;
Matches 406; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

QY 1 MPAGRRGPAQAARRPPLPLLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 60
Db 1 MPAGRRGPAQAARRPPLPLLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 60
QY 61 SVHGDPGATAGLYWTLNGRRPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
Db 61 SVHGDPGATAGLYWTLNGRRPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
QY 121 GSILAGSCLVGLPPEKPNVISCWSKNMKDLCRTWTPGAHGETFLHNTYSLKYLRYGQ 180
Db 121 GSILAGSCLVGLPPEKPNVISCWSKNMKDLCRTWTPGAHGETFLHNTYSLKYLRYGQ 180
QY 181 DNTCEEYHTVGPHSCHIPKDALFTPEIWEATNRLGARSVDLTLDILDVTTDPPPD 240
Db 181 DNTCEEYHTVGPHSCHIPKDALFTPEIWEATNRLGARSVDLTLDILDVTTDPPPD 240
QY 241 VHVSRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVESVDWKVDDVSNQTSCLAG 300
Db 241 VHVSRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVESVDWKVDDVSNQTSCLAG 300
QY 301 LKPGTVYFVQVRCNPFGIYSGKAGIWESEHPTAATPRSERPGGGGACPRGGEPSS 360
Db 301 LKPGTVYFVQVRCNPFGIYSGKAGIWESEHPTAATPRSERPGGGGACPRGGEPSS 360
QY 361 GPVRRLEKQFLGMLKGHAYCSNLSFRLYDQRAWMQSHKTRNQ---VLP 407
Db 361 GPVRRLEKQFLGMLKGHAYCSNLSFRLYDQRAWMQSHKTRNQDEGILP 410

RESULT 9
US-09-944-449-32
; Sequence 32, Application US/09944449
; Patent No. US20020102647A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein,David
; APPLICANT: Eaton,Dan
; APPLICANT: Ferrara,Napoleone
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gerritsen,Mary
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul
; APPLICANT: Grimaldi,Christopher
; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; Q ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-866-028-32

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; APPLICANT: Gurney,Austin
; APPLICANT: Hillan,Kenneth
; APPLICANT: Kljavin,Ivar
; APPLICANT: Napier,Mary
; APPLICANT: Roy,Margaret
; APPLICANT: Tumas,Daniel
; APPLICANT: Wood,William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,449
; CURRENT FILING DATE: 2001-09-26
; Prior application data removed - consult PALM or file wrapper
; Q ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-944-449-32

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RESULT 6
US-09-944-907-32
; Sequence 32, Application US/09944907
; Publication No. US20020198147A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavini, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,907
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-907-32

Query Match 98.8%; Score 2202.5; DB 9; Length 422;
Best Local Similarity 99.0%; Pred. No. 3.8e-157;
Matches 406; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

Qy 1 MPAGRRGPAAGSARRPPPLPLLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
Db 1 MPAGRRGPAAGSARRPPPLPLLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy 61 SVHGDPGATAGLYWTNGRLPPELSRVLNASTLALANLNGSRORSQDNLVCHARD 120
Db 61 SVHGDPGATAGLYWTNGRLPPELSRVLNASTLALANLNGSRORSQDNLVCHARD 120

Qy 121 GSILAGSCLYVGLPEKPVNISCSKMKDLTCRWTPGAHGETFLHTNYSKYLRLWYQ 180
Db 121 GSILAGSCLYVGLPEKPVNISCSKMKDLTCRWTPGAHGETFLHTNYSKYLRLWYQ 180

Qy 181 DNTCEEYHTVGPCHIPKDLALFTPYEIWEATNRLGARSQDNLVCHARD 240
Db 181 DNTCEEYHTVGPCHIPKDLALFTPYEIWEATNRLGARSQDNLVCHARD 240

Qy 241 VHSRVGSGLEQSLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVVDVDSNQTSCLAG 300
Db 241 VHSRVGSGLEQSLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVVDVDSNQTSCLAG 300

Qy 301 LKPGTVYFVQVRCNPFPGIYGSKKAGIWESEHPTAASTPRSERPGGGACPRGGEPS 360
Db 301 LKPGTVYFVQVRCNPFPGIYGSKKAGIWESEHPTAASTPRSERPGGGACPRGGEPS 360

Qy 361 GPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLP 407
Db 361 GPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILP 410

RESULT 7
US-09-944-929-32
; Sequence 32, Application US/09944929

Publication No. US20020197612A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavini, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,929
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-929-32

Query Match 98.8%; Score 2202.5; DB 9; Length 422;
Best Local Similarity 99.0%; Pred. No. 3.8e-157;
Matches 406; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

Qy 1 MPAGRRGPAAGSARRPPPLPLLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60
Db 1 MPAGRRGPAAGSARRPPPLPLLLLLLCVLGAPRAGSGAHTAVISPQDPTLLIGSSLLATC 60

Qy 61 SVHGDPGATAGLYWTNGRLPPELSRVLNASTLALANLNGSRORSQDNLVCHARD 120
Db 61 SVHGDPGATAGLYWTNGRLPPELSRVLNASTLALANLNGSRORSQDNLVCHARD 120

Qy 121 GSILAGSCLYVGLPEKPVNISCSKMKDLTCRWTPGAHGETFLHTNYSKYLRLWYQ 180
Db 121 GSILAGSCLYVGLPEKPVNISCSKMKDLTCRWTPGAHGETFLHTNYSKYLRLWYQ 180

Qy 181 DNTCEEYHTVGPCHIPKDLALFTPYEIWEATNRLGARSQDNLVCHARD 240
Db 181 DNTCEEYHTVGPCHIPKDLALFTPYEIWEATNRLGARSQDNLVCHARD 240

Qy 241 VHSRVGSGLEQSLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVVDVDSNQTSCLAG 300
Db 241 VHSRVGSGLEQSLSVRWVSPALKDFLFOAKYQIRYRVEDSVDMKVVDVDSNQTSCLAG 300

Qy 301 LKPGTVYFVQVRCNPFPGIYGSKKAGIWESEHPTAASTPRSERPGGGACPRGGEPS 360
Db 301 LKPGTVYFVQVRCNPFPGIYGSKKAGIWESEHPTAASTPRSERPGGGACPRGGEPS 360

Qy 361 GPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLP 407
Db 361 GPVRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILP 410

RESULT 8
US-09-866-028-32
; Sequence 32, Application US/09866028
; Patent No. US20020058309A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan

QY 361 GPVRRLEKQFLGWLKKHAYCSNLISFRLYDQWRAMQKSHKTRNQ---VLP 407
Db 361 GPVRRLEKQFLGWLKKHAYCSNLISFRLYDQWRAMQKSHKTRNQDEGILP 410

RESULT 5

US-09-944-944-32
; Sequence 32, Application US/09944944
; Patent No. US20020173463A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerriksen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: F2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,944
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/074,092
; PRIOR FILING DATE: February 9, 1998
; PRIOR APPLICATION NUMBER: 60/075,945
; PRIOR FILING DATE: February 25, 1998
; PRIOR APPLICATION NUMBER: 60/112,850
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 60/113,296
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 60/146,222
; PRIOR FILING DATE: July 28, 1999
; PRIOR APPLICATION NUMBER: PCT/US98/19330
; PRIOR FILING DATE: September 16, 1998
; PRIOR APPLICATION NUMBER: PCT/US98/25108

; PRIOR FILING DATE: December 1, 1998
; PRIOR APPLICATION NUMBER: 09/216,021
; PRIOR FILING DATE: December 16, 1998
; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-944-32

Query Match 98.8%; Score 2202.5; DB 9; Length 422;
Best Local Similarity 99.0%; Pred. No. 3.8e-157;
Matches 406; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

QY 1 MPAGRRGPAQAQARRPPPLPILLLILCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 60
Db 1 MPAGRRGPAQAQARRPPPLPILLLILCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 60

QY 61 SVHGDPGPGATAEGLYWTNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
Db 61 SVHGDPGPGATAEGLYWTNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120

QY 121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYLKRWYQ 180
Db 121 GSILAGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSLKYLKRWYQ 180

QY 181 DNTCEYHTVGPCHSCHI PKDLALFTPEYIWEATNGLSARSVDLTLDLDVVTTPPPD 240
Db 181 DNTCEYHTVGPCHSCHI PKDLALFTPEYIWEATNGLSARSVDLTLDLDVVTTPPPD 240

QY 241 VHVSRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDKVVDVDSNOTSCLAG 300
Db 241 VHVSRVGGLEDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSVDKVVDVDSNOTSCLAG 300

QY 301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSWSHPTAASTPRSERPGPGGACPRGGEPS 360
Db 301 LKPGTVYFVQVRCNPFGIYGSKKAGIWSWSHPTAASTPRSERPGPGGACPRGGEPS 360

QY 361 GPVRRLEKQFLGWLKKHAYCSNLISFRLYDQWRAMQKSHKTRNQ---VLP 407
Db 361 GPVRRLEKQFLGWLKKHAYCSNLISFRLYDQWRAMQKSHKTRNQDEGILP 410

Db 241 VHVSRVGGLEDQLSVRVVSPALLKDFLQAKYQIRYRVSDVDMKWVDDVSNQTSCLAG 300
Qy 301 LKPGTVYFVQVRCNPFGLYGSKKAGIWESEWHPHTAASPRSERPCGGGACPRGGEPS 360
Db 301 LKPGTVYFVQVRCNPFGLYGSKKAGIWESEWHPHTAASPRSERPCGGGACPRGGEPS 360
Qy 361 GPVRRLEKQFLGLWKHKHAYCSNLSRFLYDQWRAMQKSHKTRNQ---VLP 407
Db 361 GPVRRLEKQFLGLWKHKHAYCSNLSRFLYDQWRAMQKSHKTRNDEGILP 410

RESULT 4
US-09-944-896-32
Sequence 32, Application US/09944896
Patent No. US20020168715A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Guney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,896
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222

PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 32
LENGTH: 422
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-896-32

Query Match 98.8%; Score 2202.5; DB 9; Length 422;
Best Local Similarity 99.0%; Pred. No. 3.8e-157;
Matches 406; Conservative 1; Mismatches 0; Indels 3; Gaps 1;
Qy 1 MPAGRRGPAQASARRPPPLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 60
Db 1 MPAGRRGPAQASARRPPPLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 60
Qy 61 SVHGDPGATAGLYWTNGRRRLPPELSRVLNASTLALANLNGSRORSNDLVCHARD 120
Db 61 SVHGDPGATAGLYWTNGRRRLPPELSRVLNASTLALANLNGSRORSNDLVCHARD 120
Qy 121 GSILAGSCLYVGLPEKPVNISCSKMKDLTCRWTPCAHGETFLHTNYSKYKLRYGQ 180
Db 121 GSILAGSCLYVGLPEKPVNISCSKMKDLTCRWTPCAHGETFLHTNYSKYKLRYGQ 180
Qy 181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSADVLTLDLVDTVTTDPPPD 240
Db 181 DNTCEEYHTVGPHSCHIPKDLALFTPYEIWVEATNRLGARSADVLTLDLVDTVTTDPPPD 240
Qy 241 VHVSRVGGLEDQLSVRVVSPALLKDFLQAKYQIRYRVSDVDMKWVDDVSNQTSCLAG 300
Db 241 VHVSRVGGLEDQLSVRVVSPALLKDFLQAKYQIRYRVSDVDMKWVDDVSNQTSCLAG 300
Qy 301 LKPGTVYFVQVRCNPFGLYGSKKAGIWESEWHPHTAASPRSERPCGGGACPRGGEPS 360
Db 301 LKPGTVYFVQVRCNPFGLYGSKKAGIWESEWHPHTAASPRSERPCGGGACPRGGEPS 360

Db 181 DNTCEEYHTVGPCHSPKDLALFTPEIWEATNRLGARSVDLTLDLDVTTDPPD 240
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Db 241 VHSRVGGLDQLSVRVVSPALXDFLFOAKYQIRYRVESVDMKVVDVDSNOTSCRLAG 300
Qy 301 LKPGTVYFVQVRCNPFYIGYKAGIINSEMSHPTAATPRSERPGGGGACPRGGPSS 360
Db 301 LKPGTVYFVQVRCNPFYIGYKAGIINSEMSHPTAATPRSERPGGGGACPRGGPSS 360
Qy 361 GPVRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLP 407
Db 361 GPVRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNDEGILP 410

RESULT 3

US-09-944-403-32
Sequence 32, Application US/09944403
Accession No. US20020165143A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerlitsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P2548PCL1
CURRENT APPLICATION NUMBER: US/09/944, 403
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866, 028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067, 411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069, 334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069, 425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069, 696
PRIOR FILING DATE: December 16, 1997
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PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069, 702
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PRIOR APPLICATION NUMBER: 60/069, 873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068, 017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070, 440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074, 086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074, 092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075, 945

PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 32
LENGTH: 422
TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-403-32

Query Match 98.8%; Score 2202.5; DB 9; Length 422;
Best Local Similarity 99.0%; Pred. No. 3.8e-157;
Matches 406; Conservative 1; Mismatches 0; Indels 3; Gaps 1;
Qy 1 MPAGRGPAQAQARRPPPLPLLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 60
Db 1 MPAGRGPAQAQARRPPPLPLLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 60
Qy 61 SVHGDPGATAEGLYWTNGRRLLPPELSRVLNASTLALANLNGSRQSRGDNLVCHARD 120
Db 61 SVHGDPGATAEGLYWTNGRRLLPPELSRVLNASTLALANLNGSRQSRGDNLVCHARD 120
Qy 121 GSTLAGSCLYVGLPPEKPVNISCSKMKDLCRTWTPGAHGETFLHTNYSKYLKRWYQ 180
Db 121 GSTLAGSCLYVGLPPEKPVNISCSKMKDLCRTWTPGAHGETFLHTNYSKYLKRWYQ 180
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 Db 241 VHSRVGLEDQLSVRWVSPALXDFLFOAKYQIRYRVEDSVDMKVVDDVSNQTSCLAG 300
 Qy 301 LKPGTVYVQVRCNPFPGIYSGKAGIWSHPTAASRSPRSGPGGACPRGGEPS 360
 Db 301 LKPGTVYVQVRCNPFPGIYSGKAGIWSHPTAASRSPRSGPGGACPRGGEPS 360
 Qy 361 GPRRELKQFLGWLKXKHCYCNLSRLYDQWRANMOKSHKTRNQ----- 404
 Db 361 GPRRELKQFLGWLKXKHCYCNLSRLYDQWRANMOKSHKTRNQ----- 404
 Qy 405 VLPDKL 410
 Db 421 VLPDKL 426

T 2
 5-944-413-32
 ; Sequence 32, Application US/09944413
 ; Patent No. US20020156004A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin
 ; APPLICANT: Botstein, David
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul
 ; APPLICANT: Grimaldi, Christopher
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Hillan, Kenneth
 ; APPLICANT: Kljavin, Ivar
 ; APPLICANT: Napier, Mary
 ; APPLICANT: Roy, Margaret
 ; APPLICANT: Tamas, Daniel
 ; APPLICANT: Wood, William
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P2548P1C1
 ; CURRENT APPLICATION NUMBER: US/09/944,413
 ; CURRENT FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 09/866,028
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/067,411
 ; PRIOR FILING DATE: December 3, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,334
 ; PRIOR FILING DATE: December 11, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,335
 ; PRIOR FILING DATE: December 11, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,278
 ; PRIOR FILING DATE: December 11, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,425
 ; PRIOR FILING DATE: December 12, 1997
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 ; PRIOR FILING DATE: December 16, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,694
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 ; PRIOR APPLICATION NUMBER: 60/069,702
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 ; PRIOR APPLICATION NUMBER: 60/069,870
 ; PRIOR FILING DATE: December 17, 1997
 ; PRIOR APPLICATION NUMBER: 60/069,873
 ; PRIOR FILING DATE: December 17, 1997
 ; PRIOR APPLICATION NUMBER: 60/068,017
 ; PRIOR FILING DATE: December 18, 1997
 ; PRIOR APPLICATION NUMBER: 60/070,440
 ; PRIOR FILING DATE: January 5, 1998
 ; PRIOR APPLICATION NUMBER: 60/074,086

; PRIOR FILING DATE: February 9, 1998
 ; PRIOR APPLICATION NUMBER: 60/074,092
 ; PRIOR FILING DATE: February 9, 1998
 ; PRIOR APPLICATION NUMBER: 60/075,945
 ; PRIOR FILING DATE: February 25, 1998
 ; PRIOR APPLICATION NUMBER: 60/112,850
 ; PRIOR FILING DATE: December 16, 1998
 ; PRIOR APPLICATION NUMBER: 60/113,296
 ; PRIOR FILING DATE: December 22, 1998
 ; PRIOR APPLICATION NUMBER: 60/146,222
 ; PRIOR FILING DATE: July 28, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US98/19330
 ; PRIOR FILING DATE: September 16, 1998
 ; PRIOR APPLICATION NUMBER: PCT/US98/25108
 ; PRIOR FILING DATE: December 1, 1998
 ; PRIOR APPLICATION NUMBER: 09/216,021
 ; PRIOR FILING DATE: December 16, 1998
 ; PRIOR APPLICATION NUMBER: 09/218,517
 ; PRIOR FILING DATE: December 22, 1998
 ; PRIOR APPLICATION NUMBER: 09/254,311
 ; PRIOR FILING DATE: March 3, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/12252
 ; PRIOR FILING DATE: June 22, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/21090
 ; PRIOR FILING DATE: September 15, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/28409
 ; PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/28313
 ; PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/28301
 ; PRIOR FILING DATE: December 1, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US99/30095
 ; PRIOR FILING DATE: December 16, 1999
 ; PRIOR APPLICATION NUMBER: PCT/US00/03565
 ; PRIOR FILING DATE: February 11, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/04414
 ; PRIOR FILING DATE: February 22, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/05841
 ; PRIOR FILING DATE: March 2, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/08439
 ; PRIOR FILING DATE: March 30, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/14042
 ; PRIOR FILING DATE: May 22, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/20710
 ; PRIOR FILING DATE: July 28, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US00/32678
 ; PRIOR FILING DATE: December 1, 2000
 ; PRIOR APPLICATION NUMBER: PCT/US01/06520
 ; PRIOR FILING DATE: February 28, 2001
 ; NUMBER OF SEQ ID NOS: 120
 ; SEQ ID NO 32
 ; LENGTH: 422
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-09-944-413-32

Query Match 98.8%; Score 2202.5; DB 9; Length 422;
 Best Local Similarity 99.0%; Pred. No. 3.8e-157; Mismatches 0; Indels 3; Gaps 1;
 Matches 406; Conservative 1;

Qy 1 MPAGRRGPAAQASARRPPPLPLLLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 60
 Db 1 MPAGRRGPAAQASARRPPPLPLLLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 60
 Qy 61 SVHGDPGATAGLYWTNGRRRLPPELSRVLNASTLALANLNGSRORSQDNLVCHARD 120
 Db 61 SVHGDPGATAGLYWTNGRRRLPPELSRVLNASTLALANLNGSRORSQDNLVCHARD 120
 Qy 121 GSILAGSCLVYGLPEKPVNISCSKNNKDLTCRWTPCAHGETFLHTNYSKYLKRWYQ 180
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 Qy 181 DNTCEVHTVGPCHSIPKDLALFTPYBIWEATNRLGARSADVLTLILDVWTTDPPD 240

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

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Number of hits satisfying chosen parameters: 199416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
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 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
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 - 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
 - 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
 - 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
 - 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	2202.5	98.8	422	9	US-09-944-896-32
5	2202.5	98.8	422	9	US-09-944-944-32
6	2202.5	98.8	422	9	US-09-944-907-32
7	2202.5	98.8	422	9	US-09-944-929-32
8	2202.5	98.8	422	10	US-09-866-028-32
9	2202.5	98.8	422	10	US-09-944-449-32
10	2202.5	98.8	422	10	US-09-944-457-32
11	2202.5	98.8	422	10	US-09-944-862-32
12	2202.5	98.8	422	10	US-09-945-587-32
13	2202.5	98.8	422	10	US-09-945-015-32
14	2202.5	98.8	422	10	US-09-944-396-32
15	2202.5	98.8	422	10	US-09-944-097-32
16	2202.5	98.8	422	10	US-09-944-432-32
17	2202.5	98.8	422	10	US-09-943-762-32
18	2202.5	98.8	422	10	US-09-944-654-32
19	2202.5	98.8	422	10	US-09-943-851A-32

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21	2197.5	98.5	425	10	US-09-880-578-4
22	2188	98.1	421	10	US-09-037-657-44
23	2120	95.1	434	9	US-10-074-901-4
24	2114.5	94.8	413	10	US-09-037-657-13
25	2095	93.9	425	10	US-09-037-657-15
26	2088	93.6	425	10	US-09-880-578-6
27	2037	91.3	392	10	US-09-880-578-18
28	2027.5	90.9	405	9	US-10-074-901-2
29	2021	90.6	389	10	US-09-880-578-22
30	2020	90.6	389	10	US-09-880-578-28
31	2020	90.6	389	10	US-09-880-578-29
32	2019	90.5	389	10	US-09-880-578-30
33	2018	90.5	389	10	US-09-880-578-24
34	2018	90.5	389	10	US-09-880-578-25
35	2018	90.5	389	10	US-09-880-578-27
36	2017	90.4	389	10	US-09-880-578-26
37	2016.5	90.4	388	10	US-09-880-578-17
38	2016	90.4	389	10	US-09-880-578-31
39	2000.5	89.7	385	10	US-09-880-578-20
40	1963.5	88.0	385	10	US-09-880-578-19
41	1812	81.3	350	10	US-09-037-657-25
42	1687.5	75.7	544	9	US-10-056-984-3
43	1645	73.8	303	10	US-09-880-578-23
44	1641	73.6	303	10	US-09-880-578-21
45	1463	65.6	278	10	US-09-037-657-19

ALIGNMENTS

RESULT 1
US-10-056-984-2
; Sequence 2, Application US/10056984
; Publication No. US20030045683A1
; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce
; TITLE OF INVENTION: H14 DNA and Polypeptides
; FILE REFERENCE: 03260.0085-00000
; CURRENT APPLICATION NUMBER: US/10/056,984
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/392,746
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/070,885
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/00516
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-056-984-2

Query Match	99.2%	Score 2212;	DB 9;	Length 426;
Best Local Similarity	96.2%	Pred. No. 7.4e-158;		
Matches 410;	Conservative	0;	Mismatches	0;
Indels	16;	Gaps	1;	
QY	1	MPAGRRGPAQAARRPPPLLPLLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC	60	
Db	1	MPAGRRGPAQAARRPPPLLPLLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC	60	
QY	61	SVHGDPPGATAGLYWTLNGRLPPELSVLNASTLALANLNGSRQSGDNLVCHARD	120	
Db	61	SVHGDPPGATAGLYWTLNGRLPPELSVLNASTLALANLNGSRQSGDNLVCHARD	120	
QY	121	GSLTAGSCLYVGLPPEKPNVNI SCWSKNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYQG	180	
Db	121	GSLTAGSCLYVGLPPEKPNVNI SCWSKNMKDLTCRWTPGAHGETFLHTNYSKYLKRWYQG	180	
QY	181	DNTCEYHTVGHPSCHIPKDLALFTPEIWEATNRLGARSVDLTLDILDVVVTTDPPD	240	

; Sequence 29, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Presnell, Scott R.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/071,224
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 389 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-071-224-29

Query Match 90.6%; Score 2020; DB 4; Length 389;
Best Local Similarity 95.6%; Pred. No. 3.3e-188;
Matches 372; Conservative 1; Mismatches 0; Indels 16; Gaps 1;

QY 38 AHTAVISPDPTLLIGSSLLATCSVHGDPGATAGLYWTNGRRLLPPELSRVLNASTLA 97
DB 1 AHTAVISPDPTLLIGSSLLATCSVHGDPGATAGLYWTNGRRLLPPELSRVLNASTLA 60
QY 98 LALANLNGSRQSGDNLVCHARDGSLVGLPPEKPVNISCSWKMKDLTCRWTP 157
DB 61 LALANLNGSRQSGDNLVCHARDGSLVGLPPEKPVNISCSWKMKDLTCRWTP 120
QY 158 GAHGETFLHTNYSKYKLRYWGQDNTCEEYHTVGPCHSKIPKDLALFTPYEIWEATNRL 217
DB 121 GAHGETFLHTNYSKYKLRYWGQDNTCEEYHTVGPCHSKIPKDLALFTPYEIWEATNRL 180
QY 218 GSARSVDLTLDLVTTDPPDVHVSRRVGLGLEDQLSVRWVSPALXDFLFOAKYQIRYR 277
DB 181 GSARSVDLTLDLVTTDPPDVHVSRRVGLGLEDQLSVRWVSPALXDFLFOAKYQIRYR 240
QY 278 VEDSDVMKVVDDVSNQTSCLAGLKPCTVYFVQVRCNPFGLYGSKKAGIWSKSHPTAAS 337
DB 241 VEDSDVMKVVDDVSNQTSCLAGLKPCTVYFVQVRCNPFGLYGSKKAGIWSKSHPTAAS 300
QY 338 TPRSRRPGGGGACPRGSGPVRRELKQFLGWLKXAYCSNLSFRLYDQWRAMQK 397

DB 301 TPRSRRPGGGGACPRGSGPVRRELKQFLGWLKXAYCSNLSFRLYDQWRAMQK 360
QY 398 SHKTRNQ-----VLPDKL 410
DB 361 SHKTRNQHRTGSCPRADGARREVLPDKL 389
RESULT 13
US-09-071-224-30
; Sequence 30, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Presnell, Scott R.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/071,224
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 96-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 389 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-071-224-30

Query Match 90.5%; Score 2019; DB 4; Length 389;
Best Local Similarity 95.6%; Pred. No. 4.2e-188;
Matches 372; Conservative 1; Mismatches 0; Indels 16; Gaps 1;

QY 38 AHTAVISPDPTLLIGSSLLATCSVHGDPGATAGLYWTNGRRLLPPELSRVLNASTLA 97
DB 1 AHTAVISPDPTLLIGSSLLATCSVHGDPGATAGLYWTNGRRLLPPELSRVLNASTLA 60
QY 98 LALANLNGSRQSGDNLVCHARDGSLVGLPPEKPVNISCSWKMKDLTCRWTP 157
DB 61 LALANLNGSRQSGDNLVCHARDGSLVGLPPEKPVNISCSWKMKDLTCRWTP 120
QY 158 GAHGETFLHTNYSKYKLRYWGQDNTCEEYHTVGPCHSKIPKDLALFTPYEIWEATNRL 217
DB 121 GAHGETFLHTNYSKYKLRYWGQDNTCEEYHTVGPCHSKIPKDLALFTPYEIWEATNRL 180

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
APPLICATION NUMBER: US/09/071,224
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-224-22

Query Match 90.6%; Score 2021; DB 4; Length 389;
Best Local Similarity 95.9%; Pred. No. 2.7e-188;
Matches 373; Conservative 0; Mismatches 0; Indels 16; Gaps 1;

Qy 38 AHTAVISQDDPTLLIGSSLLATCSVHGDPGATAGLYWTLNGRRLPPELSRVLNASTLA 97
Db 1 AHTAVISQDDPTLLIGSSLLATCSVHGDPGATAGLYWTLNGRRLPPELSRVLNASTLA 60
Qy 98 LALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLPPEKPVNISCSWKNKMDLTCRWTP 157
Db 61 LALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLPPEKPVNISCSWKNKMDLTCRWTP 120
Qy 158 GAHGETFLHTNYSKYLRWYQDNTCEEYHTVGPCHSCHI PKDLALFPPYIWEATNRL 217
Db 121 GAHGETFLHTNYSKYLRWYQDNTCEEYHTVGPCHSCHI PKDLALFPPYIWEATNRL 180
Qy 218 GSARSDVLTLDILDVTTDPPDVHVS RVGGLDQLSVRWSPPALKDFLFOAKYQIYR 277
Db 181 GSARSDVLTLDILDVTTDPPDVHVS RVGGLDQLSVRWSPPALKDFLFOAKYQIYR 240
Qy 278 VEDSVDMKVDDVSNQTSCLRLAGLKPGTVYFVQVRCNPFPGIYGSKKAGIWEWSHPTAAS 337
Db 241 VEDSVDMKVDDVSNQTSCLRLAGLKPGTVYFVQVRCNPFPGIYGSKKAGIWEWSHPTAAS 300
Qy 338 TPRSRRPGGGACBPRGGEPSGVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQK 397
Db 301 TPRSRRPGGGACBPRGGEPSGVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQK 360
Qy 398 SHKTRNQ-----VLPDKL 410
Db 361 SHKTRNQHRTRGSCPRADGARREVLDPDKL 389

RESULT 11
US-09-071-224-28
; Sequence 28, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Presnell, Scott R.
; APPLICANT: Telmers, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehner, Joyce M.

TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics
STREET: 1201 Eastlake Ave East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,224
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX:
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-071-224-28

Query Match 90.6%; Score 2020; DB 4; Length 389;
Best Local Similarity 95.6%; Pred. No. 3.3e-188;
Matches 372; Conservative 1; Mismatches 0; Indels 16; Gaps 1;

Qy 38 AHTAVISQDDPTLLIGSSLLATCSVHGDPGATAGLYWTLNGRRLPPELSRVLNASTLA 97
Db 1 AHTAVISQDDPTLLIGSSLLATCSVHGDPGATAGLYWTLNGRRLPPELSRVLNASTLA 60
Qy 98 LALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLPPEKPVNISCSWKNKMDLTCRWTP 157
Db 61 LALANLNGSRQSGDNLVCHARDGSIILAGSCLYVGLPPEKPVNISCSWKNKMDLTCRWTP 120
Qy 158 GAHGETFLHTNYSKYLRWYQDNTCEEYHTVGPCHSCHI PKDLALFPPYIWEATNRL 217
Db 121 GAHGETFLHTNYSKYLRWYQDNTCEEYHTVGPCHSCHI PKDLALFPPYIWEATNRL 180
Qy 218 GSARSDVLTLDILDVTTDPPDVHVS RVGGLDQLSVRWSPPALKDFLFOAKYQIYR 277
Db 181 GSARSDVLTLDILDVTTDPPDVHVS RVGGLDQLSVRWSPPALKDFLFOAKYQIYR 240
Qy 278 VEDSVDMKVDDVSNQTSCLRLAGLKPGTVYFVQVRCNPFPGIYGSKKAGIWEWSHPTAAS 337
Db 241 VEDSVDMKVDDVSNQTSCLRLAGLKPGTVYFVQVRCNPFPGIYGSKKAGIWEWSHPTAAS 300
Qy 338 TPRSRRPGGGACBPRGGEPSGVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQK 397
Db 301 TPRSRRPGGGACBPRGGEPSGVRRELKQFLGWLKKHAYCSNLSFRLYDQWRAMQK 360
Qy 398 SHKTRNQ-----VLPDKL 410
Db 361 SHKTRNQHRTRGSCPRADGARREVLDPDKL 389

RESULT 12
US-09-071-224-29

Db 121 WTPGAGETFLHTNYSUKYKLRWYQDNTCEEYHTVGPHSCHIPKDALFTPYEIWYAT 180
QY 215 NRIGSARSVDLTLDLDVTTDPPDVHVSVRVGGLEDQLSVRVSPPALKDFLFOAKYQI 274
Db 181 NRIGSARSVDLTLDLDVTTDPPDVHVSVRVGGLEDQLSVRVSPPALKDFLFOAKYQI 240
QY 275 RYRVESVDWKVVDVSNQTSCLRIAGLKPGTVYFVQVRCNPFPGIYGSKKAGIWSWSHPT 334
Db 241 RYRVESVDWKVVDVSNQTSCLRIAGLKPGTVYFVQVRCNPFPGIYGSKKAGIWSWSHPT 300
QY 335 AASTPRSERPGGGACPEPGPSSGPVREIKQFLGWLKXAYCSNLFRILYDQWRAW 394
Db 301 AASTPRSERPGGGACPEPGPSSGPVREIKQFLGWLKXAYCSNLFRILYDQWRAW 360
QY 395 MQSKSHKTRNQ-----VLPDKL 410
Db 361 MQSKSHKTRNQHRTRGSCPRADGARREVLDPKL 392

RESULT 8
US-09-012-072-2
; Sequence 2, Application US/09012072
; Patent No. 6060276
; GENERAL INFORMATION:
; APPLICANT: Maslakowski, Piotr
; TITLE OF INVENTION: No. 6060276el Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/012,072
; CURRENT FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 405
; TYPE: PRT
; ORGANISM: MOUSE
US-09-012-072-2

Query Match 90.9%; Score 2027.5; DB 3; Length 405;
Best Local Similarity 95.6%; Pred. No. 6.6e-189;
Matches 370; Conservative 6; Mismatches 8; Indels 3; Gaps 1;
QY 24 LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATCSVHGDPGATAGLYWTLNGRRL 83
Db 7 LLLCVLGVPGRGSGAHTAVISPODPTLLIGSSLLQATCSIHGDTGATAGLYWTLNGRRL 66

QY 84 PPELSRVLNASTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLPPEKPNISC 143
Db 67 PSELSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLPPEKPNISC 126
QY 144 WSKNMKDLTCRWTPGAGHETFLHTNYSUKYKLRWYQDNTCEEYHTVGPHSCHIPKDAL 203
Db 127 WSRNMKDLTCRWTPGAGHETFLHTNYSUKYKLRWYQDNTCEEYHTVGPHSCHIPKDAL 186
QY 204 FTPYEIWEATNRLGARSVDLTLDLDVTTDPPDVHVSVRVGGLEDQLSVRVSPPAL 263
Db 187 FTPYEIWEATNRLGARSVDLTLDLDVTTDPPDVHVSVRVGGLEDQLSVRVSPPAL 246
QY 264 KDFLFOAKYQIRYRVESVDWKVVDVSNQTSCLRIAGLKPGTVYFVQVRCNPFPGIYGSKK 323
Db 247 KDFLFOAKYQIRYRVESVDWKVVDVSNQTSCLRIAGLKPGTVYFVQVRCNPFPGIYGSKK 306
QY 324 AGIWSWSHPTAASTPRSERPGGGACPEPGPSSGPVRRRELKQFLGWLKXAYCSNL 383
Db 307 AGIWSWSHPTAASTPRSERPGGGACPEPGPSSGPVRRRELKQFLGWLKXAYCSNL 366

QY 384 SFRLYDQWRAWMQSKSHKTRNQ---VLP 407
Db 367 SFRLYDQWRAWMQSKSHKTRNQDEGILP 393
RESULT 9
US-09-120-601-2

; Sequence 2, Application US/09120601
; Patent No. 6207413
; GENERAL INFORMATION:
; APPLICANT: Maslakowski, Piotr
; TITLE OF INVENTION: No. 6207413el Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/120,601
; CURRENT FILING DATE: 1998-07-22
; EARLIER APPLICATION NUMBER: 09/012,072
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 405
; TYPE: PRT
; ORGANISM: MOUSE
US-09-120-601-2

Query Match 90.9%; Score 2027.5; DB 4; Length 405;
Best Local Similarity 95.6%; Pred. No. 6.6e-189;
Matches 370; Conservative 6; Mismatches 8; Indels 3; Gaps 1;
QY 24 LLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATCSVHGDPGATAGLYWTLNGRRL 83
Db 7 LLLCVLGVPGRGSGAHTAVISPODPTLLIGSSLLQATCSIHGDTGATAGLYWTLNGRRL 66
QY 84 PPELSRVLNASTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLPPEKPNISC 143
Db 67 PSELSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLPPEKPNISC 126
QY 144 WSKNMKDLTCRWTPGAGHETFLHTNYSUKYKLRWYQDNTCEEYHTVGPHSCHIPKDAL 203
Db 127 WSRNMKDLTCRWTPGAGHETFLHTNYSUKYKLRWYQDNTCEEYHTVGPHSCHIPKDAL 186
QY 204 FTPYEIWEATNRLGARSVDLTLDLDVTTDPPDVHVSVRVGGLEDQLSVRVSPPAL 263
Db 187 FTPYEIWEATNRLGARSVDLTLDLDVTTDPPDVHVSVRVGGLEDQLSVRVSPPAL 246
QY 264 KDFLFOAKYQIRYRVESVDWKVVDVSNQTSCLRIAGLKPGTVYFVQVRCNPFPGIYGSKK 323
Db 247 KDFLFOAKYQIRYRVESVDWKVVDVSNQTSCLRIAGLKPGTVYFVQVRCNPFPGIYGSKK 306
QY 324 AGIWSWSHPTAASTPRSERPGGGACPEPGPSSGPVRRRELKQFLGWLKXAYCSNL 383
Db 307 AGIWSWSHPTAASTPRSERPGGGACPEPGPSSGPVRRRELKQFLGWLKXAYCSNL 366
QY 384 SFRLYDQWRAWMQSKSHKTRNQ---VLP 407
Db 367 SFRLYDQWRAWMQSKSHKTRNQDEGILP 393

RESULT 10
US-09-071-224-22
; Sequence 22, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Presnell, Scott R.
; APPLICANT: Jeimberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehnar, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTOR5
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESS: ZymoGenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA USA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:

US-09-071-224-6
 ; Sequence 6, Application US/09071224
 ; Patent No. 6271343
 ; GENERAL INFORMATION:
 ; APPLICANT: Lok, Si
 ; APPLICANT: Presnell, Scott R.
 ; APPLICANT: Jelmsberg, Anna C.
 ; APPLICANT: Gilbert, Teresa
 ; APPLICANT: Foster, Donald C.
 ; APPLICANT: Adams, Robyn L.
 ; APPLICANT: Lehner, Joyce M.
 ; TITLE OF INVENTION: MAMMALIAN ZCYTORS
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Zymogenetics
 ; STREET: 1201 Eastlake Ave East
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98102
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/071,224
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lunn, Paul G
 ; REGISTRATION NUMBER: 32,743
 ; REFERENCE/DOCKET NUMBER: 96-22
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-442-6627
 ; TELEFAX: 206-442-6678
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 425 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; 9-071-224-6

Query Match 93.6%; Score 2088; DB 4; Length 425;
 Best Local Similarity 93.5%; Pred. No. 9.3e-195;
 Matches 386; Conservative 7; Mismatches 14; Indels 6; Gaps 2;
 Qy 1 MPAGRRGPAAGSARPPPLPL---LLLCVLPAPRAGSGAHTAVISPDPTLLIGSLL 57
 Db 1 MPAGGPGPAAGSARPPRRLSSLLSPLLLCVLGPQGSGAHTAVISPDPTLLIGSLH 60
 Qy 58 ATCSVHGDPGPGATAGLYWTNGRLPPELSRVLNASTLALALANLNGSRORSQGNLVCH 117
 Db 61 ATCSIHGDTGPGATAGLYWTNGRLPPELSRVLNASTLALALANLNGSRORSQGNLVCH 120
 Qy 118 ARDGSIIAGSCLYVGLPEKPVNISCKNMDLTCRWTPCAHGETFLHTNYSKYKLWR 177
 Db 121 ARDGSIIAGSCLYVGLPEKPFNISCKRNKMDLTCRWTPCAHGETFLHTNYSKYKLWR 180
 Qy 178 YGQNTCEEYHTVGPCHSPKDLALFTPYEIIWEATNRLGARSADSVLTLDLDVTTDP 237
 Db 181 YGQNTCEEYHTVGPCHSPKDLALFTPYEIIWEATNRLGARSADSVLTLDLDVTTDP 240
 Qy 238 PPDVHVS RVGGLDQLSVRVVSPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSR 297
 Db 241 PPDVHVS RVGGLDQLSVRVVSPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSR 300

Qy 298 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSHSHPTAATPSRSPRGGGACPRGGE 357
 Db 301 LAGLKPGTVYFVQVRCNPFGIYGSKKAGIWSHSHPTAATPSRSPRGGGACPRGGE 360
 Qy 358 PSSGPRRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLP 407
 Db 361 PSSGPRRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILP 413

RESULT 7
 US-09-071-224-18
 ; Sequence 18, Application US/09071224
 ; Patent No. 6271343
 ; GENERAL INFORMATION:
 ; APPLICANT: Lok, Si
 ; APPLICANT: Presnell, Scott R.
 ; APPLICANT: Jelmsberg, Anna C.
 ; APPLICANT: Gilbert, Teresa
 ; APPLICANT: Foster, Donald C.
 ; APPLICANT: Adams, Robyn L.
 ; APPLICANT: Lehner, Joyce M.
 ; TITLE OF INVENTION: MAMMALIAN ZCYTORS
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Zymogenetics
 ; STREET: 1201 Eastlake Ave East
 ; CITY: Seattle
 ; STATE: WA
 ; COUNTRY: USA
 ; ZIP: 98102
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/071,224
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lunn, Paul G
 ; REGISTRATION NUMBER: 32,743
 ; REFERENCE/DOCKET NUMBER: 96-22
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-442-6627
 ; TELEFAX: 206-442-6678
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 392 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-071-224-18

Query Match 91.3%; Score 2037; DB 4; Length 392;
 Best Local Similarity 95.9%; Pred. No. 7.5e-190;
 Matches 376; Conservative 0; Mismatches 0; Indels 16; Gaps 1;
 Qy 35 GSGAHTAVISPDPTLLIGSLLATCSVHGDPGATAGLYWTNGRLPPELSRVLNAS 94
 Db 1 GSGAHTAVISPDPTLLIGSLLATCSVHGDPGATAGLYWTNGRLPPELSRVLNAS 60
 Qy 95 TLALALANLNGSRORSQGNLVCHARDGSIILAGSCLYVGLPEKPVNISCKNMDLTCR 154
 Db 61 TLALALANLNGSRORSQGNLVCHARDGSIILAGSCLYVGLPEKPVNISCKNMDLTCR 120
 Qy 155 WTPGAHGETFLHTNYSKYKLRYWYQDNTCEEYHTVGPCHSPKDLALFTPYEIIWEAT 214

QY 1 MPAGRRGPAASARRPPPLPLLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 60
DB 1 MPAGRRGPAASARRPPPLPLLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 60
QY 61 SVHGDPPGATAEGLYWTNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
DB 61 SVHGDPPGATAEGLYWTNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
QY 121 GSILAGSCLYVGLPPEKPNVISCWSNMKDLTCRWTPGAHGETFLHTNYSCLKRWYQG 180
DB 121 GSILAGSCLYVGLPPEKPNVISCWSNMKDLTCRWTPGAHGETFLHTNYSCLKRWYQG 180
QY 181 DNTCEYHTVGPCHSCHIPKDLALFTPEIWEATNRLGARSVDLTLDLDVGHSLPLPS 231
DB 181 DNTCEYHTVGPCHSCHIPKDLALFTPEIWEATNRLGARSVDLTLDLDVGHSLPLPS 240
QY 232 -----VTTDPPDVHVSRRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRV 278
DB 241 PATPGLSLLVRGKVVTDDPPDVHVSRRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRV 300
QY 279 EDSVDWKVDDVSNQTSCLAGLKPGTVFVQVRCNPFPGIYGSKKAGIWEWSHPTAAS 338
DB 301 EDSVDWKVDDVSNQTSCLAGLKPGTVFVQVRCNPFPGIYGSKKAGIWEWSHPTAAS 360
QY 339 PRSERPGGGACEPRGGPSSGPVRELLKQFLGWLKHKHAYCSNLSFRLYDQWRAMWQKS 398
DB 361 PRSERPGGGACEPRGGPSSGPVRELLKQFLGWLKHKHAYCSNLSFRLYDQWRAMWQKS 420
QY 399 HKTRNQ-----VLPDKL 410
DB 421 HKTRNQHRTGSCPRADGARREVLDPKL 448

RESULT 4
US-09-012-072-4
; Sequence 4, Application US/09012072
; Patent No. 6060276
; GENERAL INFORMATION:
; APPLICANT: Masiakowski, Piotr
; TITLE OF INVENTION: No. 6060276el Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/012, 072
; EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 434
; TYPE: PRT
; ORGANISM: HUMAN
US-09-012-072-4

Query Match 95.1%; Score 2120; DB 3; Length 434;
Best Local Similarity 91.2%; Pred. No. 7.4e-198;
Matches 396; Conservative 0; Mismatches 0; Indels 38; Gaps 2;

QY 15 RPPPLPLLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATCSVHGDPGATAEGL 74
DB 1 RPPPLPLLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATCSVHGDPGATAEGL 60
QY 75 YWTLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 134
DB 61 YWTLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 120
QY 135 PEKPNVISCWSNMKDLTCRWTPGAHGETFLHTNYSCLKRWYGDNTCEEYHTVGPHS 194
DB 121 PEKPNVISCWSNMKDLTCRWTPGAHGETFLHTNYSCLKRWYGDNTCEEYHTVGPHS 180
QY 195 CHIPKDLALFTPEIWEATNRLGARSVDLTLDLDVGHSLPLPSPATPGLSLLVRGKV 232
DB 181 CHIPKDLALFTPEIWEATNRLGARSVDLTLDLDVGHSLPLPSPATPGLSLLVRGKV 240
QY 233 VTTDPPDVHVSRRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVSDSVDMKVDDVSN 292

DB 241 VTTDPPDVHVSRRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVSDSVDMKVDDVSN 300
QY 293 QTSCLAGLKPGTVFVQVRCNPFPGIYGSKKAGIWEWSHPTAASPRSERPGGGACE 352
DB 301 QTSCLAGLKPGTVFVQVRCNPFPGIYGSKKAGIWEWSHPTAASPRSERPGGGACE 360
QY 353 PRGGPSSGPVRELLKQFLGWLKHKHAYCSNLSFRLYDQWRAMWQSKHKTNRQ----- 404
DB 361 PRGGPSSGPVRELLKQFLGWLKHKHAYCSNLSFRLYDQWRAMWQSKHKTNRQHRTGSCP 420
QY 405 -----VLPDKL 410
DB 421 RADGARREVLDPKL 434
RESULT 5
US-09-120-601-4
; Sequence 4, Application US/09120601
; Patent No. 6207413
; GENERAL INFORMATION:
; APPLICANT: Masiakowski, Piotr
; TITLE OF INVENTION: No. 6207413el Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/120, 601
; CURRENT FILING DATE: 1998-07-22
; EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 434
; TYPE: PRT
; ORGANISM: HUMAN
US-09-120-601-4

Query Match 95.1%; Score 2120; DB 4; Length 434;
Best Local Similarity 91.2%; Pred. No. 7.4e-198;
Matches 396; Conservative 0; Mismatches 0; Indels 38; Gaps 2;

QY 15 RPPPLPLLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATCSVHGDPGATAEGL 74
DB 1 RPPPLPLLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATCSVHGDPGATAEGL 60
QY 75 YWTLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 134
DB 61 YWTLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 120
QY 135 PEKPNVISCWSNMKDLTCRWTPGAHGETFLHTNYSCLKRWYGDNTCEEYHTVGPHS 194
DB 121 PEKPNVISCWSNMKDLTCRWTPGAHGETFLHTNYSCLKRWYGDNTCEEYHTVGPHS 180
QY 195 CHIPKDLALFTPEIWEATNRLGARSVDLTLDLDVGHSLPLPSPATPGLSLLVRGKV 232
DB 181 CHIPKDLALFTPEIWEATNRLGARSVDLTLDLDVGHSLPLPSPATPGLSLLVRGKV 240
QY 233 VTTDPPDVHVSRRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVSDSVDMKVDDVSN 292
DB 241 VTTDPPDVHVSRRVGGLEDQLSVRWVSPALKDFLFOAKYQIRYRVSDSVDMKVDDVSN 300
QY 293 QTSCLAGLKPGTVFVQVRCNPFPGIYGSKKAGIWEWSHPTAASPRSERPGGGACE 352
DB 301 QTSCLAGLKPGTVFVQVRCNPFPGIYGSKKAGIWEWSHPTAASPRSERPGGGACE 360
QY 353 PRGGPSSGPVRELLKQFLGWLKHKHAYCSNLSFRLYDQWRAMWQSKHKTNRQ----- 404
DB 361 PRGGPSSGPVRELLKQFLGWLKHKHAYCSNLSFRLYDQWRAMWQSKHKTNRQHRTGSCP 420
QY 405 -----VLPDKL 410
DB 421 RADGARREVLDPKL 434

RESULT 6

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Query Match      98.6%; Score 2198.5; DB 4; Length 422;
Best Local Similarity 98.8%; Pred. No. 1.6e-205;
Matches 405; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

Qy 1 MPAGRRGPAAGSARRPPPLLLLLLVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 60
Db 1 MPAGRRGPAAGSARRPPPLLLLLLVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 60
Qy 61 SVHGDPGPGATAEGLYWTINGRRLLPELSRVLNASTLALANLNGSRORSQDNLVCHARD 120
Db 61 SVHGDPGPGATAEGLYWTINGRRLLPELSRVLNASTLALANLNGSRORSQDNLVCHARD 120
Qy 121 GSILAGSCLYVGLPEKPVNISCSWKMKDLTCRWTPCAHGETFLHTNYSKYKLRWYQ 180
Db 121 GSILAGSCLYVGLPEKPVNISCSWKMKDLTCRWTPCAHGETFLHTNYSKYKLRWYQ 180
Qy 181 DNTCEEYHTVGPCHSPKDLALFTPYEIWEATNRLGARSVDLTLDILDVTTDPPD 240
Db 181 DNTCEEYHTVGPCHSPKDLALFTPYEIWEATNRLGARSVDLTLDILDVTTDPPD 240
Qy 241 VHSRVGGLDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSDVKWVDDVSNQTSCLAG 300
Db 241 VHSRVGGLDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSDVKWVDDVSNQTSCLAG 300
Qy 301 LKPGTVYFVQVRCNPPFGIYGSKKAGIWESEWHSHTAASTPRSERPGGGGACPRGEPSS 360
Db 301 LKPGTVYFVQVRCNPPFGIYGSKKAGIWESEWHSHTAASTPRSERPGGGGACPRGEPSS 360
Qy 361 GPVRELKQFLGWLKHKHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLP 407
Db 361 GPVRELKQFLGWLKHKHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILP 410

RESULT 2
US-09-071-224-4
; Sequence 4, Application US/09071224
; Patent No. 6271343
; GENERAL INFORMATION:
; APPLICANT: Lok, Si
; APPLICANT: Presnelli, Scott R.
; APPLICANT: Jelmeberg, Anna C.
; APPLICANT: Gilbert, Teresa
; APPLICANT: Foster, Donald C.
; APPLICANT: Adams, Robyn L.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: MAMMALIAN ZCYTORS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Zymogenetics
; STREET: 1201 Eastlake Ave East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,224
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: 98-22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6627
```

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TELEFAX: 206-442-6678
TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-071-224-4

Query Match      98.5%; Score 2197.5; DB 4; Length 425;
Best Local Similarity 96.0%; Pred. No. 2.1e-205;
Matches 409; Conservative 0; Mismatches 0; Indels 17; Gaps 2;

Qy 1 MPAGRRGPAAGSARRPPPLLLLLLVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 60
Db 1 MPAGRRGPAAGSARRPPPLLP-LLLLVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 59
Qy 61 SVHGDPGPGATAEGLYWTINGRRLLPELSRVLNASTLALANLNGSRORSQDNLVCHARD 120
Db 60 SVHGDPGPGATAEGLYWTINGRRLLPELSRVLNASTLALANLNGSRORSQDNLVCHARD 119
Qy 121 GSILAGSCLYVGLPEKPVNISCSWKMKDLTCRWTPCAHGETFLHTNYSKYKLRWYQ 180
Db 120 GSILAGSCLYVGLPEKPVNISCSWKMKDLTCRWTPCAHGETFLHTNYSKYKLRWYQ 179
Qy 181 DNTCEEYHTVGPCHSPKDLALFTPYEIWEATNRLGARSVDLTLDILDVTTDPPD 240
Db 180 DNTCEEYHTVGPCHSPKDLALFTPYEIWEATNRLGARSVDLTLDILDVTTDPPD 239
Qy 241 VHSRVGGLDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSDVKWVDDVSNQTSCLAG 300
Db 240 VHSRVGGLDQLSVRWVSPPALKDFLFOAKYQIRYRVEDSDVKWVDDVSNQTSCLAG 299
Qy 301 LKPGTVYFVQVRCNPPFGIYGSKKAGIWESEWHSHTAASTPRSERPGGGGACPRGEPSS 360
Db 300 LKPGTVYFVQVRCNPPFGIYGSKKAGIWESEWHSHTAASTPRSERPGGGGACPRGEPSS 359
Qy 361 GPVRELKQFLGWLKHKHAYCSNLSFRLYDQWRAMQKSHKTRNQ----- 404
Db 360 GPVRELKQFLGWLKHKHAYCSNLSFRLYDQWRAMQKSHKTRNQHRTRGSCPRADGARRE 419
Qy 405 VLPDKL 410
Db 420 VLPDKL 425

RESULT 3
US-09-120-601-6
; Sequence 6, Application US/09120601
; Patent No. 6207413
; GENERAL INFORMATION:
; APPLICANT: Maslowski, Piotr
; TITLE OF INVENTION: No. 6207413el Orphan Receptors
; FILE REFERENCE: REG 630
; CURRENT APPLICATION NUMBER: US/09/120,601
; CURRENT FILING DATE: 1998-07-22
; EARLIER APPLICATION NUMBER: 09/012,072
; EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 448
; TYPE: PRT
; ORGANISM: HUMAN
US-09-120-601-6

Query Match      98.3%; Score 2191; DB 4; Length 448;
Best Local Similarity 91.5%; Pred. No. 9.6e-205;
Matches 410; Conservative 0; Mismatches 0; Indels 38; Gaps 2;
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GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: March 13, 2003, 11:41:12 ; Search time 43.296 Seconds
(without alignments)
1261.843 Million cell updates/sec

Title: US-09-521-335-12

Perfect score: 2230

Sequence: 1 MPAGRRGPAQAARRPPPL.....WRAWQKSHKTRNQVLDPKL 410

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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 - 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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 - 11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
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 - 13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
 - 14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
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 - 19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
 - 20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
 - 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
 - 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
 - 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2230	100.0	410	20	AA29779 Human DNAX soluble
2	2230	100.0	410	21	AA19568 Human cytokine-lik
3	2230	100.0	410	22	AA19567 Human cytokine rec
4	2212	99.2	426	20	AA29781 Amino acid sequenc
5	2202.5	98.8	422	20	AA29781 Human U4 haematopo
6	2202.5	98.8	422	20	AA29781 Human tumour-assoc
7	2202.5	98.8	422	20	AA17825 Human PRO327 prote
8	2202.5	98.8	422	20	AA29781 Human type 1 cytot
9	2202.5	98.8	422	21	AA29781 Amino acid sequenc
10	2202.5	98.8	422	21	AA29781 Human PRO327 polyp

11	2202.5	98.8	422	22	AA29781 Amino acid sequenc
12	2200	98.7	445	23	AA29781 Amino acid sequenc
13	2200	98.7	457	23	AA29781 Human NS protein s
14	2198.5	98.6	422	20	AA29781 Human Zcytor5 prot
15	2197.5	98.5	425	20	AA29781 Allelic variant of
16	2191	98.3	448	21	AA29781 Human orphan cytot
17	2188	98.1	421	22	AA29781 Murine haemopoiet
18	2181.5	95.6	408	19	AA29781 Amino acid sequenc
19	2131.5	95.6	408	20	AA29781 Human U4 haematopo
20	2131.5	95.6	408	20	AA29781 Amino acid sequenc
21	2114.5	94.8	413	19	AA29781 Novel haemopoietin
22	2114.5	94.8	413	19	AA29781 A murine hemopoiet
23	2114.5	94.8	413	22	AA29781 Murine haemopoiet
24	2095	93.9	425	19	AA29781 Novel haemopoietin
25	2095	93.9	425	19	AA29781 A murine hemopoiet
26	2095	93.9	425	22	AA29781 Murine haemopoiet
27	2091	93.8	425	19	AA29781 Nucleotide sequenc
28	2091	93.8	425	20	AA29781 Murine U4 haematop
29	2088	93.6	425	20	AA29781 Rat Zcytor5 protei
30	2037	91.3	392	20	AA29781 Human Zcytor5 vari
31	2028.5	91.0	416	20	AA29781 Mouse DNAX soluble
32	2027.5	90.9	405	20	AA29781 Amino acid sequenc
33	2027.5	90.9	405	21	AA29781 Mouse orphan cytot
34	2021	90.6	389	20	AA29781 Human Zcytor5 vari
35	2020	90.6	389	20	AA29781 Human Zcytor5 vari
36	2020	90.6	389	20	AA29781 Human Zcytor5 vari
37	2019	90.5	389	20	AA29781 Human Zcytor5 vari
38	2018	90.5	389	20	AA29781 Human Zcytor5 vari
39	2018	90.5	389	20	AA29781 Human Zcytor5 vari
40	2018	90.5	389	20	AA29781 Human Zcytor5 vari
41	2017	90.4	389	20	AA29781 Human Zcytor5 vari
42	2016.5	90.4	388	20	AA29781 Human Zcytor5 vari
43	2016	90.4	389	20	AA29781 Human Zcytor5 vari
44	2014	90.3	407	21	AA29781 Mouse cytokine-lik
45	2014	90.3	407	22	AA29781 Mouse cytokine rec

ALIGNMENTS

RESULT 1

AA29779

ID AA29779 standard; Protein; 410 AA.

XX AA29779;

DT 04-NOV-1999 (first entry)

XX Human DNAX soluble receptor subunit 1.

XX DNAX soluble receptor subunit 1; DNAX cytokine receptor subunit 1;
interleukin B30; DSR1; DCR1; IL-B30; cytokine receptor; diagnosis;
inflammatory disorder; inflammatory response; innate immunity;
morphogenic development; immunological disorder.

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

PT New receptor subunits useful in the treatment of inflammatory disorders
XX Claim 2; Page 22-23; 133pp; English.
XX The present invention describes a composition (I) comprising DNAX
CC cytokine receptor subunit 1 (CDRS1) protein and DNAX soluble receptor
CC subunit 1 (CDRS1) protein, which together encode a new mammalian
CC cytokine-related receptor (R), or DCRS1 and interleukin B30 (IL-B30)
CC proteins, or DCRS1 and IL-B30 proteins. (I) comprising DCRS1 and DCRS1
CC is useful for screening for ligands (i.e. agonists/antagonists) from
CC a library of compounds, which are useful for modulating the physiology
CC or development of a cell or tissue culture e.g. inflammatory responses,
CC innate immunity and/or morphogenic development. (R), antibodies and
CC ligands are useful for treatment of conditions, especially immunological
CC disorders, associated with conditions exhibiting abnormal immunological
CC (R). (R) is useful as a phosphate labeling enzyme to label substrates.
CC and the subunits DCRS1 and DCRS1 are useful as immunogens for generating
CC antibodies, or as antigens for binding antibodies. Nucleic acids
CC encoding (R) are useful for identifying related DNAs and mRNAs, and
CC variants from other individuals or species. The present sequence
CC represents the specifically claimed human DCRS1, for use in the
CC composition of the present invention.
XX
SQ Sequence 410 AA;
Query Match 100.0%; Score 2230; DB 20; Length 410;
Best Local Similarity 100.0%; Pred. No. 3.3e-181; Indels 0; Gaps 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPAGRRGPAQAQARRPPPLPPLLLLCVLGAPRAGSGAHTAVISQDPTLLIGSSLLATC 60
Db 1 MPAGRRGPAQAQARRPPPLPPLLLLCVLGAPRAGSGAHTAVISQDPTLLIGSSLLATC 60
Qy 61 SVHGDPPGATAEGLYWTLNRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
Db 61 SVHGDPPGATAEGLYWTLNRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
Qy 121 GSILAGSCLYVGLPEKPNWSCNKNMKDLTCRWTGPAHGETFLHTNYSKYKLRWYQG 180
Db 121 GSILAGSCLYVGLPEKPNWSCNKNMKDLTCRWTGPAHGETFLHTNYSKYKLRWYQG 180
Qy 181 DNTCEEYHTVGPCHIPKDALFTPEIWEATNRLGARSADVLTLDLVDTTDPDPPD 240
Db 181 DNTCEEYHTVGPCHIPKDALFTPEIWEATNRLGARSADVLTLDLVDTTDPDPPD 240
Qy 241 VHSRVGGLDQLSVRWVSPALKDFLFOAKYQIRYRVEDSDWKVDDVSNQTSCLAG 300
Db 241 VHSRVGGLDQLSVRWVSPALKDFLFOAKYQIRYRVEDSDWKVDDVSNQTSCLAG 300
301 LKPGTVYFQVRCNPFYIGSKKAGTWSEWSHPTAASPRSRPFGGACPRGGEPS 360
301 LKPGTVYFQVRCNPFYIGSKKAGTWSEWSHPTAASPRSRPFGGACPRGGEPS 360
Qy 361 GPVRELKQFLGWLKHYACNSLFRYLDQWRAWMQKSHKTRNQVLDPKL 410
Db 361 GPVRELKQFLGWLKHYACNSLFRYLDQWRAWMQKSHKTRNQVLDPKL 410
RESULT 2
AAB19588
ID AAB19588 standard; Protein; 410 AA.
XX AAB19588;
XX
XX 22-JAN-2001 (first entry)
XX Human cytokine-like factor-1.
XX Cytokine-like factor-1; CLF-1; interleukin-B60; IL-B60; human;
KW cytokine; receptor; neuron; inflammation; antiinflammatory;
KW autoimmune disease; therapy.
XX
OS Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..38
FT /label= Signal_peptide
FT Protein 39..410
FT /label= Mature_protein
FT Domain 39..130
FT /note= "Ig-like domain"
FT Domain 131..237
FT /note= "Ig-like domain"
FT Domain 238..410
FT /note= "Ig-like domain"
XX W0200053631-A1.
XX 14-SEP-2000;
XX 09-MAR-2000; 2000WO-US06182.
XX 11-MAR-1999; 99US-0267901.
XX (SCHE) SCHERING CORP.
XX Oppmann B, Timans JC, Kastelein RA, Bazan JF;
XX WPI; 2000-587426/55.
XX Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,
PT polypeptides, and nucleic acids, useful in research, diagnosis and for
PT treating inflammatory and autoimmune disorders -
XX Claim 1; Page 21-22; 97pp; English.
XX The present sequence is that of human cytokine-like factor-1
CC (CLF-1), a cytokine receptor family protein, which forms a complex
CC with human interleukin-B60 (IL-B60, see AAB19586). The IL-B60/CLF-1
CC cytokine serves as a key physiological factor in motor neuron
CC development and regeneration. A claimed soluble complex comprises
CC at least 6 amino acids of mature IL-60B, at least 6 amino acids of
CC mature CLF-1 or at least 6 amino acids of mature CNTF-R. A claimed
CC method of modulating the physiology or development of a cell or
CC tissue culture cell involves contacting the cell with an agonist or
CC antagonist of a complex comprising IL-60B and CLF-1 or CNTF-R. A
CC claimed method of screening for a receptor which binds the complex
CC involves contacting the complex with a cell expressing the receptor,
CC to form a detectable interaction resulting in a physiological
CC response in the cell.
XX SQ Sequence 410 AA;
Query Match 100.0%; Score 2230; DB 21; Length 410;
Best Local Similarity 100.0%; Pred. No. 3.3e-181; Indels 0; Gaps 0;
Matches 410; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MPAGRRGPAQAQARRPPPLPPLLLLCVLGAPRAGSGAHTAVISQDPTLLIGSSLLATC 60
Db 1 MPAGRRGPAQAQARRPPPLPPLLLLCVLGAPRAGSGAHTAVISQDPTLLIGSSLLATC 60
Qy 61 SVHGDPPGATAEGLYWTLNRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
Db 61 SVHGDPPGATAEGLYWTLNRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
Qy 121 GSILAGSCLYVGLPEKPNWSCNKNMKDLTCRWTGPAHGETFLHTNYSKYKLRWYQG 180
Db 121 GSILAGSCLYVGLPEKPNWSCNKNMKDLTCRWTGPAHGETFLHTNYSKYKLRWYQG 180
Qy 181 DNTCEEYHTVGPCHIPKDALFTPEIWEATNRLGARSADVLTLDLVDTTDPDPPD 240
Db 181 DNTCEEYHTVGPCHIPKDALFTPEIWEATNRLGARSADVLTLDLVDTTDPDPPD 240
Qy 241 VHSRVGGLDQLSVRWVSPALKDFLFOAKYQIRYRVEDSDWKVDDVSNQTSCLAG 300
Db 241 VHSRVGGLDQLSVRWVSPALKDFLFOAKYQIRYRVEDSDWKVDDVSNQTSCLAG 300

Query Match 99.2%; Score 2212; DB 20; Length 426;
 Best Local Similarity 96.2%; Pred. No. 1.2e-179;
 Matches 410; Conservative 0; Mismatches 0; Indels 16; Gaps 1;

QY 1 MPAGRRGPAQAQARRPPPLPLLLLLVCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 60
 DB 1 MPAGRRGPAQAQARRPPPLPLLLLLVCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 60
 QY 61 SVHGDPGATAEGLYWTNGRRLLPELSRVLNASTLALANLNGSRORSQDNLVCHARD 120
 DB 61 SVHGDPGATAEGLYWTNGRRLLPELSRVLNASTLALANLNGSRORSQDNLVCHARD 120
 QY 121 GSILAGSCLYVGLPPEKPVNISCSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQ 180
 DB 121 GSILAGSCLYVGLPPEKPVNISCSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQ 180
 QY 181 DNTCEEYHTVGPCHSCHIPKDALFTPYEIWEATNRLGSARSDVLTLDILDVTTDPPPD 240
 DB 181 DNTCEEYHTVGPCHSCHIPKDALFTPYEIWEATNRLGSARSDVLTLDILDVTTDPPPD 240
 QY 241 VHSRVGLEDQLSVRWVSPALKDFLQAKYQIRYRVESVDWKVDDVSNQTSCLAG 300
 DB 241 VHSRVGLEDQLSVRWVSPALKDFLQAKYQIRYRVESVDWKVDDVSNQTSCLAG 300
 QY 301 LKPGTVYFVQVRCNPFPGIYGSKKAGIWESEHPTAASTPRSERPGCGGACEPRGGEPS 360
 DB 301 LKPGTVYFVQVRCNPFPGIYGSKKAGIWESEHPTAASTPRSERPGCGGACEPRGGEPS 360
 QY 361 GPVRELKQFLGWLKXKHCYCSNLSFRLYDQWRAMQSKHKTNRQ----- 404
 DB 361 GPVRELKQFLGWLKXKHCYCSNLSFRLYDQWRAMQSKHKTNRQ----- 404
 QY 405 VLPDKL 410
 DB 421 VLPDKL 426

RESULT 5
 AAY26339
 ID AAY26339 standard; Protein; 422 AA.
 XX AC AAY26339;
 XX DT 13-JAN-2000 (first entry)
 XX DE Human U4 haematopoietin receptor superfamily chain-2.
 XX

Human U4 protein; haematopoietin receptor superfamily;
 biological activity; cytokine; cell proliferation; cell differentiation;
 immune stimulation; immune suppression; haematopoiesis regulation;
 immune disorder; immune deficiency; autoimmune disorder; allergy; cancer;
 myeloid cell; lymphoid cell deficiency; platelet disorder.
 OS Homo sapiens.
 XX WO9953066-A1.
 XX PD 21-OCT-1999.
 XX PF 09-APR-1999; 99WO-US07882.
 XX PR 10-APR-1998; 98US-0058660.
 XX PA (GEM) GENETICS INST INC.
 XX PI Collins M, Donaldson D, Neben T, Whitters M;
 XX WPI: 1999-611303/52.
 XX N-PSDB: AAX90754.
 XX Novel polypeptides and polynucleotides used for treatment of human
 PT diseases and disorders e.g. immune disorders or deficiencies caused by

PT fungal, parasitic or viral infections -
 XX Claim 9; Pages 36-38; 43pp; English.
 XX CC The present sequence is a human U4 protein which is a member of
 CC haematopoietin receptor superfamily.
 CC The protein is predicted to have the following biological
 CC activities: cytokine, cell proliferation/differentiation, immune
 CC stimulating or suppressing and haematopoiesis regulating. The U4
 CC protein can be used to treat immune disorders and deficiencies.
 CC autoimmune disorders, allergies, cancer, myeloid or lymphoid cell
 CC deficiencies and platelet disorders.
 XX SQ Sequence 422 AA;
 Query Match 98.8%; Score 2202.5; DB 20; Length 422;
 Best Local Similarity 99.0%; Pred. No. 7.6e-179;
 Matches 406; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

QY 1 MPAGRRGPAQAQARRPPPLPLLLLLVCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 60
 DB 1 MPAGRRGPAQAQARRPPPLPLLLLLVCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 60
 QY 61 SVHGDPGATAEGLYWTNGRRLLPELSRVLNASTLALANLNGSRORSQDNLVCHARD 120
 DB 61 SVHGDPGATAEGLYWTNGRRLLPELSRVLNASTLALANLNGSRORSQDNLVCHARD 120
 QY 121 GSILAGSCLYVGLPPEKPVNISCSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQ 180
 DB 121 GSILAGSCLYVGLPPEKPVNISCSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQ 180
 QY 181 DNTCEEYHTVGPCHSCHIPKDALFTPYEIWEATNRLGSARSDVLTLDILDVTTDPPPD 240
 DB 181 DNTCEEYHTVGPCHSCHIPKDALFTPYEIWEATNRLGSARSDVLTLDILDVTTDPPPD 240
 QY 241 VHSRVGLEDQLSVRWVSPALKDFLQAKYQIRYRVESVDWKVDDVSNQTSCLAG 300
 DB 241 VHSRVGLEDQLSVRWVSPALKDFLQAKYQIRYRVESVDWKVDDVSNQTSCLAG 300
 QY 301 LKPGTVYFVQVRCNPFPGIYGSKKAGIWESEHPTAASTPRSERPGCGGACEPRGGEPS 360
 DB 301 LKPGTVYFVQVRCNPFPGIYGSKKAGIWESEHPTAASTPRSERPGCGGACEPRGGEPS 360
 QY 361 GPVRELKQFLGWLKXKHCYCSNLSFRLYDQWRAMQSKHKTNRQ---VLP 407
 DB 361 GPVRELKQFLGWLKXKHCYCSNLSFRLYDQWRAMQSKHKTNRQDEGILP 410

RESULT 6
 AAY06479
 ID AAY06479 standard; Protein; 422 AA.
 XX AC AAY06479;
 XX DT 27-SEP-1999 (first entry)
 XX DE Human tumour-associated protein PRO327.
 XX KW PRO327; UNQ288; cancer; tumour; diagnosis; therapy; human.
 XX OS Homo sapiens.
 XX PN WO9935170-A2.
 XX PD 15-JUL-1999.
 XX PF 05-JAN-1999; 99WO-US00106.
 XX PR 20-NOV-1998; 98US-0109304.
 XX PR 05-JAN-1998; 98US-0070440.
 XX PR 23-APR-1998; 98US-0083500.
 XX PR 22-MAY-1998; 98US-0086414.
 XX PR 10-JUN-1998; 98US-0088742.

PR 10-NOV-1998; 98US-0107783.
 XX (GETH) GENENTECH INC.
 PA Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;
 XX Roy MA, Wood WI;
 PI WPI; 1999-430385/36.
 XX N-PSDB; AAX87256.
 DR Antibody against proteins expressed in neoplastic cells, useful for
 XX tumor diagnosis and treatment
 PT Example 1; Fig 6; 162pp; English.
 XX This sequence represents human PRO327 (UNQ288), a 46.3 kDa protein
 CC (pi 9.42) encoded by the novel cDNA clone DNA38113 (see AAX87256).
 CC Amplification of DNA38113 occurs in various lung and colon tumours
 CC and cell lines, suggesting a significant role in tumour formation
 CC and growth. Antagonists (e.g. antibodies) directed against PRO327
 CC are expected to have utility in cancer therapy. The invention
 CC identifies 14 genes (see AAX87254-67) that are amplified in the
 CC genome of tumour cells. Such amplification is expected to be
 CC associated with overexpression of the gene product and to contribute
 CC to tumorigenesis. The encoded proteins (see AAY06477-90) may be
 CC useful targets for the diagnosis and/or treatment (including
 CC prevention) of certain cancers, and may act as predictors of the
 CC prognosis of tumour treatment. Antibodies that bind the proteins
 CC are claimed and used in claimed cancer diagnostic kits.
 XX Sequence 422 AA;
 SQ
 Query Match 98.8%; Score 2202.5; DB 20; Length 422;
 Best Local Similarity 99.0%; Pred. No. 7.6e-179;
 Matches 406; Conservative 1; Mismatches 0; Indels 3; Gaps 1;
 QY 1 MPAGRRGPAQAQARRPPPLPLLLLLVCVLPAGPRAGSAGHTAVISPDPTLLIGSSLLATC 60
 DB 1 MPAGRRGPAQAQARRPPPLPLLLLLVCVLPAGPRAGSAGHTAVISPDPTLLIGSSLLATC 60
 QY 61 SVHGDPGPGATAEGLYWTNGRRLLPPELPSRVLNASTLALANLNGSRQSGDNLVCHARD 120
 DB 61 SVHGDPGPGATAEGLYWTNGRRLLPPELPSRVLNASTLALANLNGSRQSGDNLVCHARD 120
 QY 121 GSILAGSCLYVGLPPEKPVNISCSKMKDLTCRWTPGAHGETFLHTNYSIKYKLRWYGQ 180
 DB 121 GSILAGSCLYVGLPPEKPVNISCSKMKDLTCRWTPGAHGETFLHTNYSIKYKLRWYGQ 180
 QY 181 DNTCEEYHTVGPCHSCHIPKDLALFTPYEIWEATNRLGARSQSDVLTLDLDVTTDPPPD 240
 DB 181 DNTCEEYHTVGPCHSCHIPKDLALFTPYEIWEATNRLGARSQSDVLTLDLDVTTDPPPD 240
 QY 241 VHSRVGGLLEDQLSVRWVSPALKDFLFOAKYQIRYRVSDVWKVYDDVSNQTSCLAG 300
 DB 241 VHSRVGGLLEDQLSVRWVSPALKDFLFOAKYQIRYRVSDVWKVYDDVSNQTSCLAG 300
 QY 301 LKPGTVFVQVRCNPFGIYGSKKAGIWEWSHPTAASRPRSGPGGACPRGGEPS 360
 DB 301 LKPGTVFVQVRCNPFGIYGSKKAGIWEWSHPTAASRPRSGPGGACPRGGEPS 360
 QY 361 GPRVRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQ--VLP 407
 DB 361 GPRVRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILP 410
 RESULT 7
 ID AAY17825
 XX AAY17825 standard; Protein; 422 AA.
 AC AAY17825;
 XX 12-AUG-1999 (first entry)
 DT
 XX

DE Human PRO327 protein sequence.
 XX Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
 KW secreted protein; transmembrane protein; inflammation disorder.
 XX Homo sapiens.
 OS WO9928462-A2.
 XX 10-JUN-1999.
 PD 01-DEC-1998; 98WO-US25108.
 XX 25-FEB-1998; 98US-0075945.
 PR 03-DEC-1997; 97US-0067411.
 PR 11-DEC-1997; 97US-0069278.
 PR 11-DEC-1997; 97US-0069334.
 PR 11-DEC-1997; 97US-0069335.
 PR 12-DEC-1997; 97US-0069425.
 PR 16-DEC-1997; 97US-0069694.
 PR 16-DEC-1997; 97US-0069696.
 PR 17-DEC-1997; 97US-0069870.
 PR 17-DEC-1997; 97US-0069873.
 PR 18-DEC-1997; 97US-0068017.
 PR 05-JAN-1998; 98US-0070440.
 PR 09-FEB-1998; 98US-0074086.
 PR 09-FEB-1998; 98US-0074092.
 XX (GETH) GENENTECH INC.
 PA Baker KP, Chen J, Goddard A, Gurney AL, Wood WI;
 XX Yuan J;
 PI WPI; 1999-371118/31.
 XX N-PSDB; AAX80050.
 DR Nucleic acids encoding PRO secreted and transmembrane proteins
 XX Claim 12; Fig 17; 123pp; English.
 PS The present invention describes nucleic acids encoding PRO secreted and
 CC transmembrane proteins used therapeutically. The PRO proteins have
 CC cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive
 CC activity. The proteins and polynucleotides can be used in therapy,
 CC identification of homologues, raising antibodies and design of probes
 CC and primers. They can be used in a range of diseases related to proteins
 CC that they have homology with, e.g. a PRO protein having homology to
 CC complement proteins may be used in inflammatory responses.
 XX Sequence 422 AA;
 SQ
 Query Match 98.8%; Score 2202.5; DB 20; Length 422;
 Best Local Similarity 99.0%; Pred. No. 7.6e-179;
 Matches 406; Conservative 1; Mismatches 0; Indels 3; Gaps 1;
 QY 1 MPAGRRGPAQAQARRPPPLPLLLLLVCVLPAGPRAGSAGHTAVISPDPTLLIGSSLLATC 60
 DB 1 MPAGRRGPAQAQARRPPPLPLLLLLVCVLPAGPRAGSAGHTAVISPDPTLLIGSSLLATC 60
 QY 61 SVHGDPGPGATAEGLYWTNGRRLLPPELPSRVLNASTLALANLNGSRQSGDNLVCHARD 120
 DB 61 SVHGDPGPGATAEGLYWTNGRRLLPPELPSRVLNASTLALANLNGSRQSGDNLVCHARD 120
 QY 121 GSILAGSCLYVGLPPEKPVNISCSKMKDLTCRWTPGAHGETFLHTNYSIKYKLRWYGQ 180
 DB 121 GSILAGSCLYVGLPPEKPVNISCSKMKDLTCRWTPGAHGETFLHTNYSIKYKLRWYGQ 180
 QY 181 DNTCEEYHTVGPCHSCHIPKDLALFTPYEIWEATNRLGARSQSDVLTLDLDVTTDPPPD 240
 DB 181 DNTCEEYHTVGPCHSCHIPKDLALFTPYEIWEATNRLGARSQSDVLTLDLDVTTDPPPD 240
 QY 241 VHSRVGGLLEDQLSVRWVSPALKDFLFOAKYQIRYRVSDVWKVYDDVSNQTSCLAG 300

|||||
Db 241 VHSRVGLEDQLSVRWVSPALKDFLQAKYQIRYRVSDVMKWVDDVSNQTSCLAG 300
QY 301 LKPGTVYFVQVRCNPFYIGSKKAGIWEWSHPTAASTPRSERPCGGGACPRGGPSS 360
Db 301 LKPGTVYFVQVRCNPFYIGSKKAGIWEWSHPTAASTPRSERPCGGGACPRGGPSS 360
QY 361 GPVRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLP 407
Db 361 GPVRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILP 410

RESULT 8
AAV05782
ID AAY05782 standard; Protein; 422 AA.
AC AAY05782;
XX
XX 02-AUG-1999 (first entry)
XX Human type 1 cytokine receptor GBRI-ILR.
KW GBRI-ILR; hGBR-ILR; cytokine receptor; human; cancer; obesity;
KW inflammation; septic shock; AIDS; embryo development;
KW lung infection; cytostatic; anorectic; immunosuppressive;
KW antibacterial; antiviral; antiinflammatory; therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..37
FT /note= "signal peptide"
FT Protein 38..422
FT /note= "mature protein; a polypeptide comprising
FT amino acids 38-422 is also claimed in Claim
FT 1a"
XX
XX W09920755-A2.
XX
XX 29-APR-1999.
XX
XX 14-OCT-1998; 98WO-EP06497.
XX
XX 16-OCT-1997; 97GB-0021961.
XX
XX (GLAX) GLAXO GROUP LTD.
XX
XX Elson G, Gauchat J, Kosco-Vilbois M;
XX
XX WPI; 1999-288305/24.
XX N-PSDB; AAX25489.
XX
XX Novel human or mouse type I cytokine receptors hGBRI-ILR or
XX mGBRI-ILR, useful for treating e.g. cancer, immune disorders,
XX obesity and AIDS
XX
XX Claim 1a; Fig 4; 41pp; English.

XX
XX The present sequence represents a novel type I cytokine receptor
XX that has been termed human GBRI-ILR as it is believed to be an
XX interleukin receptor, or at least a substantial part of such a
XX receptor. The sequence is predicted from an isolated full-length
XX cDNA clone (see AAX25489) obtained from a human placental cDNA
XX library. GBRI-ILR mRNA is expressed most strongly in spleen,
XX thymus, lymph node, appendix, bone marrow, thyroid, adrenal
XX cortex, stomach, heart, placenta and skeletal muscle, suggesting a
XX role for GBRI-ILR in the immune system. In human foetal tissue,
XX strong expression is seen in the lung, but not in brain, kidney or
XX liver. A GBRI-ILR receptor has also been identified in mice (see
XX AAY05783). The high degree of conservation of amino acids between
XX the human and murine polypeptides indicates that this receptor is
XX functionally important. GBRI-ILR polypeptides, nucleic acids,
XX antibodies, agonists and antagonists can be used to treat e.g.

CC cancer, immune disorders, obesity (in view of homology to the
CC leptin receptor), embryonic developmental disorders, AIDS, septic
CC shock and lung infection (Claimed).
XX
SQ Sequence 422 AA;
Query Match 98.8%; Score 2202.5; DB 20; Length 422;
Best Local Similarity 99.0%; Pred. No. 7.6e-179;
Matches 406; Conservative 1; Mismatches 0; Indels 3; Gaps 1;
QY 1 MPAGRRGPAAGSARRPPPLPALLLCVLCAPRAGSGAHTAVISPODPTLLIGSSLLATC 60
Db 1 MPAGRRGPAAGSARRPPPLPALLLCVLCAPRAGSGAHTAVISPODPTLLIGSSLLATC 60
QY 61 SVHGDPGATAGLYWTLNGRRLLPPELSRVINASTLALANLNGSRQSGDNLVCHARD 120
Db 61 SVHGDPGATAGLYWTLNGRRLLPPELSRVINASTLALANLNGSRQSGDNLVCHARD 120
QY 121 GSILAGSCLYVGLPPEKPVNISCSNMKDLTCRWTPGAHGETFLHTNYSLKYLRYGQ 180
Db 121 GSILAGSCLYVGLPPEKPVNISCSNMKDLTCRWTPGAHGETFLHTNYSLKYLRYGQ 180
QY 181 DNTCEEVHTVGHPSCHIPKDLALFTPYEIVWEATNRLGARSVDLTLDLDVVTDDPPD 240
Db 181 DNTCEEVHTVGHPSCHIPKDLALFTPYEIVWEATNRLGARSVDLTLDLDVVTDDPPD 240
QY 241 VHSRVGLEDQLSVRWVSPALKDFLQAKYQIRYRVSDVMKWVDDVSNQTSCLAG 300
Db 241 VHSRVGLEDQLSVRWVSPALKDFLQAKYQIRYRVSDVMKWVDDVSNQTSCLAG 300
QY 301 LKPGTVYFVQVRCNPFYIGSKKAGIWEWSHPTAASTPRSERPCGGGACPRGGPSS 360
Db 301 LKPGTVYFVQVRCNPFYIGSKKAGIWEWSHPTAASTPRSERPCGGGACPRGGPSS 360
QY 361 GPVRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQ---VLP 407
Db 361 GPVRELKQFLGWLKHHAYCSNLSFRLYDQWRAMQKSHKTRNQDEGILP 410

RESULT 9
AAV93686
ID AAY93686 standard; Protein; 422 AA.
XX
XX AAY93686;
XX
XX 03-OCT-2000 (first entry)
XX
XX Amino acid sequence of novel polypeptide PRO327.
XX
XX PRO201; PRO292; PRO327; PRO1265; PRO344; PRO347; PRO357;
XX PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell;
XX tumorigenesis; cancer; neoplastic cell growth; cell proliferation.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..30
FT /note= "signal sequence"
FT Modified-site 3..7
FT /note= "amidation site"
FT Modified-site 30..36
FT /note= "N-myristoylation site"
FT Modified-site 37..43
FT /note= "N-myristoylation site"
FT Modified-site 44..48
FT /note= "casein kinase II phosphorylation site"
FT Modified-site 73..79
FT /note= "N-myristoylation site"
FT Modified-site 79..83
FT /note= "amidation site"
FT Modified-site 92..96
FT /note= "N-glycosylation site"
FT Modified-site 104..108

PT and Huntington's, obesity and cancer -
 PS Claim 2; Page 63-64; 67pp; French.
 XX The present sequence represents a human CLF-1 protein. The specification
 CC describes a complex comprising a NNT-1 protein and a CLF-1 and/or
 CC sCNTFRalpha protein. The NNT-1/CLF-1 complex is used to modulate
 CC activity of the sCNTFRalpha/gp130/LiFRbeta receptor complex, or to
 CC induce phosphorylation of the tyrosine of gp130 and LiFRbeta,
 CC particularly where cells expressing the receptor complex are in the
 CC central or peripheral nervous system, in neurons implicated in
 CC neuro-muscular function or in skeletal muscle. The complex or
 CC antibodies are also used to decrease the survival, growth or
 CC proliferation of tumour cells or to facilitate the proliferation and/or
 CC inhibit differentiation of cells stocks. The complex is also used to
 CC modulate activity of the gp130/LiFRbeta receptor or cells expressing
 CC that receptor, particularly those cells implicated in the immune,
 CC haematopoietic, nervous or reproductive system, the liver or skeletal
 CC muscle. Molecules of the invention may be used to prevent or treat
 CC neurodegenerative diseases including amyotrophic lateral sclerosis,
 CC Parkinson's and Huntington's disease, to repair or regenerate nervous
 CC or muscular tissue or to maintain muscular mass in paralysis patients.
 CC They may also be used to treat cancer, obesity and associated diseases,
 CC and to improve fertility, particularly to avoid endometriosis and/or
 CC assist blastocyst implantation, thrombosis, or retinal disease,
 CC particular retinal pigmentosis.
 XX
 SQ Sequence 422 AA;
 Query Match 98.8%; Score 2202.5; DB 22; Length 422;
 Best Local Similarity 99.0%; Pred. No. 7.6e-179;
 Matches 406; Conservative 1; Mismatches 0; Indels 3; Gaps 1;
 QY 1 MPAGRGPAQAQARRPPPLPLLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 60
 DB 1 MPAGRGPAQAQARRPPPLPLLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 60
 QY 61 SVHGDPGPGATAEGLYWTLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
 DB 61 SVHGDPGPGATAEGLYWTLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
 QY 121 GSILAGSCLVGLPPEKPNVISCWKNMKTLCRWTPGAHGETFLHTNYSKYLRYGQ 180
 DB 121 GSILAGSCLVGLPPEKPNVISCWKNMKTLCRWTPGAHGETFLHTNYSKYLRYGQ 180
 QY 181 DNTCEEVHTVGPCHIPKDLALFTPYEIVWEATNRLGARSVDLTLDIDVVTTPPPD 240
 DB 181 DNTCEEVHTVGPCHIPKDLALFTPYEIVWEATNRLGARSVDLTLDIDVVTTPPPD 240
 QY 241 VHSYRVGGLEDQLSVRWVSPALKDFLQAKYQIRYRVEDSDVMKVVDVSNQTSCLRLAG 300
 DB 241 VHSYRVGGLEDQLSVRWVSPALKDFLQAKYQIRYRVEDSDVMKVVDVSNQTSCLRLAG 300
 QY 301 LKPGTGVFVQVRCNPGIYGSKAGIWESEHPTAASRPRPGCGGACPRGGEPPS 360
 DB 301 LKPGTGVFVQVRCNPGIYGSKAGIWESEHPTAASRPRPGCGGACPRGGEPPS 360
 QY 361 GPVRRLEKQFLGWLKHHAYCSNLSFRLYDQWRAMWQKSHTRNQ---VLP 407
 DB 361 GPVRRLEKQFLGWLKHHAYCSNLSFRLYDQWRAMWQKSHTRNQDEGILP 410
 RESULT 12
 ID AAG63544
 XX AAG63544 standard; Protein; 445 AA.
 AC AAG63544;
 XX AAG63544;
 DT 15-OCT-2001 (first entry)
 XX
 DE Amino acid sequence of a human CLF-1 protein.
 XX
 KW NNT-1; CLF-1; sCNTFRalpha; nervous system; neuron; nervous system;

KW neuro-muscular function; tumour; immune system; haematopoietic system;
 KW reproductive system; liver; skeletal muscle; neurodegenerative disease;
 KW amyotrophic lateral sclerosis; Parkinson's disease; Huntington's disease;
 KW muscular mass; paralysis; cancer; Obesity; fertility; endometriosis;
 KW blastocyst implantation; thrombosis; retinal disease;
 KW retinal pigmentosis.
 XX Homo sapiens.
 OS
 PN WO200155172-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 26-JAN-2001; 2001WO-PR00253.
 XX
 PR 27-JAN-2000; 2000FR-0001035.
 PR 12-OCT-2000; 2000FR-0013089.
 XX
 PA (FABR) FABRE MEDICAMENT SA PIERRE.
 PA (INRM) INERM INST NAT SANTE & RECH MEDICALE.
 XX
 PI Elson G, Gauchat J, Plun-Favreau H, Chevalier S, Gascan H;
 XX
 XX WPI: 2001-488773/53.
 DR N-PSDB; AAH74485.
 DR
 XX
 PT A complex comprising a NNT-1 protein and a CLF-1 and/or sCNTFRalpha
 PT protein useful to treat neurodegenerative disease including Parkinson's
 PT and Huntington's, obesity and cancer -
 PS Claim 2; Page 60-61; 67pp; French.
 XX
 CC The present sequence represents a human CLF-1 protein. The specification
 CC describes a complex comprising a NNT-1 protein and a CLF-1 and/or
 CC sCNTFRalpha protein. The NNT-1/CLF-1 complex is used to modulate
 CC activity of the sCNTFRalpha/gp130/LiFRbeta receptor complex, or to
 CC induce phosphorylation of the tyrosine of gp130 and LiFRbeta,
 CC particularly where cells expressing the receptor complex are in the
 CC central or peripheral nervous system, in neurons implicated in
 CC neuro-muscular function or in skeletal muscle. The complex or
 CC antibodies are also used to decrease the survival, growth or
 CC proliferation of tumour cells or to facilitate the proliferation and/or
 CC inhibit differentiation of cells stocks. The complex is also used to
 CC modulate activity of the gp130/LiFRbeta receptor or cells expressing
 CC that receptor, particularly those cells implicated in the immune,
 CC haematopoietic, nervous or reproductive system, the liver or skeletal
 CC muscle. Molecules of the invention may be used to prevent or treat
 CC neurodegenerative diseases including amyotrophic lateral sclerosis,
 CC Parkinson's and Huntington's disease, to repair or regenerate nervous
 CC or muscular tissue or to maintain muscular mass in paralysis patients.
 CC They may also be used to treat cancer, obesity and associated diseases,
 CC and to improve fertility, particularly to avoid endometriosis and/or
 CC assist blastocyst implantation, thrombosis, or retinal disease,
 CC particular retinal pigmentosis.
 XX
 SQ Sequence 445 AA;
 Query Match 98.7%; Score 2200; DB 22; Length 445;
 Best Local Similarity 100.0%; Pred. No. 1.3e-178;
 Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPAGRGPAQAQARRPPPLPLLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 60
 DB 1 MPAGRGPAQAQARRPPPLPLLLLCVLGAPRAGSGAHTAVISPDPTLLIGSSLLATC 60
 QY 61 SVHGDPGPGATAEGLYWTLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
 DB 61 SVHGDPGPGATAEGLYWTLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
 QY 121 GSILAGSCLVGLPPEKPNVISCWKNMKTLCRWTPGAHGETFLHTNYSKYLRYGQ 180
 DB 121 GSILAGSCLVGLPPEKPNVISCWKNMKTLCRWTPGAHGETFLHTNYSKYLRYGQ 180

QY 181 DNTCEEYHTVGPCHSPKDLALFTPEIWEATNRLGARSVDLTLDLDVWTTDPPD 240
 Db 181 DNTCEEYHTVGPCHSPKDLALFTPEIWEATNRLGARSVDLTLDLDVWTTDPPD 240
 QY 241 VHSRVGLEDQLSVRWVSPALKDFLFOAKYQIRYRVESDVKWVDVDSNQTSCLAG 300
 Db 241 VHSRVGLEDQLSVRWVSPALKDFLFOAKYQIRYRVESDVKWVDVDSNQTSCLAG 300
 QY 301 LKPGTVYFVQVRCNPFYIGSKAGIWEWSHPTAASPRERPGGGACPRGGEPSS 360
 Db 301 LKPGTVYFVQVRCNPFYIGSKAGIWEWSHPTAASPRERPGGGACPRGGEPSS 360
 QY 361 GPVRELKQFLGWLKKHAYCSNLSFRLYDOWRAMWQKSHKTRNQ 404
 Db 361 GPVRELKQFLGWLKKHAYCSNLSFRLYDOWRAMWQKSHKTRNQ 404

RESULT 13
 ID ABB06125 standard; Protein; 457 AA.
 QY ABB06125;
 DT 10-MAY-2002 (first entry)
 DE Human NS protein sequence SEQ ID NO:217.
 KW Human; cytostatic; osteopathic; gynaecological; neuroprotective;
 KW antineuritic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV;
 KW vasotrophic; antiarteriosclerotic; antiinflammatory; dermatological;
 KW anorectic; muscular; antiinfertility; cardiovascular; anticoagulant;
 KW antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant;
 KW anticonvulsant; antidiabetic; tranquiliser; antidepressant; neuroleptic;
 KW gastrointestinal; virucide; antiulcer; cerebroprotective; nootropic;
 KW contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia;
 KW endometriosis; degenerative disease; multiple sclerosis; psoriasis;
 KW rheumatoid arthritis; catarract; restenosis; atherosclerosis; glaucoma;
 KW inflammation; skin disorder; obesity; muscular dystrophy; AIDS;
 KW ischaemia; asthma; immune disease; coagulation disease; hypertension;
 KW diabetes; anxiety; depression; schizophrenia; viral disease; stroke;
 KW gastric ulcer; Alzheimer's disease.
 OS Homo sapiens.
 XX WO200206315-A2.
 XX 24-JAN-2002.
 XX 17-JUL-2001; 2001WO-IL00653.
 PR 18-JUL-2000; 2000IL-0137345.
 PR 15-DEC-2000; 2000IL-0140354.
 XX (COMP-) COMPUEN LTD.
 XX Mintz L, Freilich S, Bernstein J;
 XX WPI; 2002-155037/20.
 DR N-PSDB; ABL39779.
 XX One hundred and twenty eight novel nucleic acid sequences, useful for
 PT treating and diagnosing e.g. cancer, asthma and Alzheimer's -
 XX Claim 6; Page 253-254; 290pp; English.
 PS ABL39691 to ABL39818 represent novel human nucleic acid sequences
 CC encoding the proteins given in ABB06037 to ABB06164. The novel sequences
 CC (NS) can have cytostatic, osteopathic, gynaecological, neuroprotective,
 CC antineuritic, antiarthritic, antipsoriatic, ophthalmological, virucide,
 CC vasotrophic, antiarteriosclerotic, antiinflammatory, dermatological,
 CC anorectic, muscular, anti-HIV, antiinfertility, cardiovascular,
 CC anticoagulant, antifibrinolytic, hypotension, antiasthmatic, cardiant,

CC immunomodulator, anticonvulsant, antidiabetic, tranquilliser, antiulcer,
 CC antipressant, gastrointestinal, neuroleptic, cerebroprotective,
 CC nootropic and contraceptive activities. The NS can be used in vaccines,
 CC gene therapy and antisense therapy. Nucleic acids, expression vectors and
 CC antibodies from the present invention can be used for treating and
 CC diagnosing e.g. cancer, osteoporosis, endometriosis, degenerative
 CC diseases, dystonia, multiple sclerosis, rheumatoid arthritis, psoriasis,
 CC cataracts, restenosis, atherosclerosis, inflammation, skin disorders,
 CC glaucoma, obesity, muscular dystrophy, AIDS, infertility, cardiovascular
 CC disease, coagulation disease, ischaemia, hypertension, asthma, immune
 CC disease, epilepsy, angina, neurodegeneration, diabetes, anxiety,
 CC depression, schizophrenia, viral disease, gastric ulcers, stroke,
 CC Alzheimer's disease and as a contraceptive.
 XX SQ Sequence 457 AA;
 Query Match 98.7%; Score 2200; DB 23; Length 457;
 Best Local Similarity 100.0%; Pred. No. 1.4e-178;
 Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MPAGRRGPAQAASARRPPPLPLLLLLCVLGAPRAGSAGHTAVISPDPTLLIGSSLLATC 60
 Db 1 MPAGRRGPAQAASARRPPPLPLLLLLCVLGAPRAGSAGHTAVISPDPTLLIGSSLLATC 60
 QY 61 SVHGDPGATAEGLYTLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
 Db 61 SVHGDPGATAEGLYTLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
 QY 121 GSILAGSCLVGLPPEKPNVISCWKNMKDLTCRWTPGAHGETFLHTNYSKYLRYWQ 180
 Db 121 GSILAGSCLVGLPPEKPNVISCWKNMKDLTCRWTPGAHGETFLHTNYSKYLRYWQ 180
 QY 181 DNTCEEYHTVGPCHSPKDLALFTPEIWEATNRLGARSVDLTLDLDVWTTDPPD 240
 Db 181 DNTCEEYHTVGPCHSPKDLALFTPEIWEATNRLGARSVDLTLDLDVWTTDPPD 240
 QY 241 VHSRVGLEDQLSVRWVSPALKDFLFOAKYQIRYRVESDVKWVDVDSNQTSCLAG 300
 Db 241 VHSRVGLEDQLSVRWVSPALKDFLFOAKYQIRYRVESDVKWVDVDSNQTSCLAG 300
 QY 301 LKPGTVYFVQVRCNPFYIGSKAGIWEWSHPTAASPRERPGGGACPRGGEPSS 360
 Db 301 LKPGTVYFVQVRCNPFYIGSKAGIWEWSHPTAASPRERPGGGACPRGGEPSS 360
 QY 361 GPVRELKQFLGWLKKHAYCSNLSFRLYDOWRAMWQKSHKTRNQ 404
 Db 361 GPVRELKQFLGWLKKHAYCSNLSFRLYDOWRAMWQKSHKTRNQ 404

RESULT 14
 AAW70860
 ID AAW70860 standard; Protein; 422 AA.
 XX AAW70860;
 XX 17-MAR-1999 (first entry)
 DT Human Zcytor5 protein sequence.
 DE Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
 KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
 KW cardiac pathology; heart enlargement; Zcytor5 ligand.
 XX Homo sapiens.
 OS WO9849307-A1.
 PN 05-NOV-1998.
 XX 01-MAY-1998; 98WO-US08865.
 XX 13-FEB-1998; 98US-0074721.
 PR 01-MAY-1997; 97US-0045287.

PR 01-MAY-1997; 97US-0850030.
XX 13-FEB-1998; 98US-0023890.
PA (ZYMO) ZYMOGENETICS INC.
XX Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM;
PI Lok S, Presnell SR, Whitmore TE;
XX WPI; 1999-034662/03.
DR N-PSDB; AAV70894.
XX New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
PT down-regulating Zcytor5 natural ligands or detecting cardiostrophin-1
PT in blood
XX Claim 1; Page 66-67; 55pp; English.
XX The present sequence represents a protein designated Zcytor5, which is
CC a cytokinin-like receptor. Soluble Zcytor5 may be administered to
CC down-regulate the effects of a growth and/or maintenance factor in
CC thyroid, heart, and skeletal muscle for example to lessen the effect
CC of cardiostrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcytor5 could be used to detect cardiostrophin-1 in the
CC blood, and to discover other possible Zcytor5 ligands. A probe
CC comprising Zcytor5 DNA or RNA can be used to determine the presence
CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify Zcytor5 and
CC therapeutically to modify Zcytor5 ligand effects.
XX Sequence 422 AA;

Query Match 98.6%; Score 2198.5; DB 20; Length 422;
Best Local Similarity 98.8%; Pred. No. 1.7e-178;
Matches 405; Conservative 2; Mismatches 0; Indels 3; Gaps 1;
QY 1 MPAGRRGPAQAARRPPPLPPLLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 60
DB 1 MPAGRRGPAQAARRPPPLPPLLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 60
QY 61 SVHGDPGPAAGLTYLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
DB 61 SVHGDPGPAAGLTYLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
QY 121 GSILAGSCLVGLPPEKPNVISCWKNMKDLTCRWTPGAHGETFLHTNYSKYLRYGQ 180
DB 121 GSILAGSCLVGLPPEKPNVISCWKNMKDLTCRWTPGAHGETFLHTNYSKYLRYGQ 180
QY 181 DNTCEEYHTVGPHSCHIPKDALFTPEIWEATNRLGARSVDLTDLDVVTTPPPD 240
DB 181 DNTCEEYHTVGPHSCHIPKDALFTPEIWEATNRLGARSVDLTDLDVVTTPPPD 240
QY 241 VHVSRVGGLEDQLSVRWSPALKDFLFOAKYQIRYRVEDSDVKVVDVSNQTSCLAG 300
DB 241 VHVSRVGGLEDQLSVRWSPALKDFLFOAKYQIRYRVEDSDVKVVDVSNQTSCLAG 300
QY 301 LKPGTVYFVQVRCNPFGIYGSKKAGIWEWSHPTAASTPRSERPGGGACERGGPSS 360
DB 301 LKPGTVYFVQVRCNPFGIYGSKKAGIWEWSHPTAASTPRSERPGGGACERGGPSS 360
QY 361 GPVRELKQFLGWLKHHAYCSNLSFRLYDQWRAMWQSHKTRNQ---VLP 407
DB 361 GPVRELKQFLGWLKHHAYCSNLSFRLYDQWRAMWQSHKTRNQDEGILP 410

RESULT 15
AAW70861
ID AAW70861 standard; Protein; 425 AA.
XX
AC AAW70861;
XX
DT 17-MAR-1999 (first entry)
XX
DE Allelic variant of human Zcytor5.

XX Zcytor5; cytokinin-like receptor; down-regulation; growth factor;
KW maintenance factor; thyroid; heart; skeletal muscle; cardiostrophin-1;
KW cardiac pathology; heart enlargement; Zcytor5 ligand; allelic variant.
XX Homo sapiens.
XX WO9849307-A1.
XX 05-NOV-1998.
XX 01-MAY-1998; 98WO-US08865.
XX 13-FEB-1998; 98US-0074721.
PR 01-MAY-1997; 97US-0045287.
PR 01-MAY-1997; 97US-0850030.
PR 13-FEB-1998; 98US-0023890.
XX (ZYMO) ZYMOGENETICS INC.
PA Adams RL, Foster DC, Gilbert T, Jelmsberg AC, Lehner JM;
PI Lok S, Presnell SR, Whitmore TE;
XX WPI; 1999-034662/03.
DR N-PSDB; AAV70895.
XX New mammalian cytokinin-like receptor Zcytor5 - useful for, e.g.
PT down-regulating Zcytor5 natural ligands or detecting cardiostrophin-1
PT in blood
XX Claim 1; Page 71-72; 55pp; English.
XX The present sequence represents an allelic variant of protein designated
CC Zcytor5, which is a cytokinin-like receptor. Soluble Zcytor5 may be
CC administered to down-regulate the effects of a growth and/or maintenance
CC factor in thyroid, heart, and skeletal muscle for example to lessen the
CC effect of cardiostrophin-1 on cardiac pathologies, so preventing heart
CC enlargement. Zcytor5 could be used to detect cardiostrophin-1 in the
CC blood, and to discover other possible Zcytor5 ligands. A probe
CC comprising Zcytor5 DNA or RNA can be used to determine the presence
CC and integrity of the Zcytor5 gene on chromosome 19. Antibodies and the
CC anti-idiotypic antibody could be used to purify Zcytor5 and
CC therapeutically to modify Zcytor5 ligand effects.
XX Sequence 425 AA;

Query Match 98.5%; Score 2197.5; DB 20; Length 425;
Best Local Similarity 96.0%; Pred. No. 2e-178;
Matches 409; Conservative 0; Mismatches 0; Indels 17; Gaps 2;
QY 1 MPAGRRGPAQAARRPPPLPPLLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 60
DB 1 MPAGRRGPAQAARRPPPLPPLLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATC 59
QY 61 SVHGDPGPAAGLTYLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 120
DB 61 SVHGDPGPAAGLTYLNGRRLLPPELSRVLNASTLALANLNGSRQSGDNLVCHARD 119
QY 121 GSILAGSCLVGLPPEKPNVISCWKNMKDLTCRWTPGAHGETFLHTNYSKYLRYGQ 180
DB 120 GSILAGSCLVGLPPEKPNVISCWKNMKDLTCRWTPGAHGETFLHTNYSKYLRYGQ 179
QY 181 DNTCEEYHTVGPHSCHIPKDALFTPEIWEATNRLGARSVDLTDLDVVTTPPPD 240
DB 180 DNTCEEYHTVGPHSCHIPKDALFTPEIWEATNRLGARSVDLTDLDVVTTPPPD 239
QY 241 VHVSRVGGLEDQLSVRWSPALKDFLFOAKYQIRYRVEDSDVKVVDVSNQTSCLAG 300
DB 240 VHVSRVGGLEDQLSVRWSPALKDFLFOAKYQIRYRVEDSDVKVVDVSNQTSCLAG 299
QY 301 LKPGTVYFVQVRCNPFGIYGSKKAGIWEWSHPTAASTPRSERPGGGACERGGPSS 360
DB 300 LKPGTVYFVQVRCNPFGIYGSKKAGIWEWSHPTAASTPRSERPGGGACERGGPSS 359

Qy	361	GPVRELKQFLGWLKKHAYCSNLSFPLYDQRAWMQSKHKTRNQ-----	404
Db	360	GPVRELKQFLGWLKKHAYCSNLSFPLYDQRAWMQSKHKTRNQHRTRGSCPRADGARRE	419

Db 360 G P V R R E L K Q F L G W L K K H A Y C S N L S F R L Y D Q W R A W M Q K S H K T R N Q H R T R G S C P P R A D G A R R E 419

QY 405 VLPDKL 410

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